

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization International Bureau



(43) International Publication Date
1 April 2004 (01.04.2004)

PCT

(10) International Publication Number
WO 2004/026888 A2

(51) International Patent Classification⁷:

C07H

(72) Inventors; and

(21) International Application Number:

PCT/US2003/029577

(75) Inventors/Applicants (for US only): LIPFORD, Grayson, B. [US/US]; 38 Bates Road, Watertown, MA 02472 (US). MOOKHERJEE, Neeloffer [IN/CA]; Apt 408, 2233 Allison Road,, Vancouver, BC V6T 1T7 (CA). BABIUK, Lorne [CA/CA]; 245 East Place, Saskatoon, Saskatchewan S7J 2Y1 (CA). BROWNLIE, Robert [CA/CA]; 123 O'Brien Crescent, Saskatoon, Saskatchewan S7K 5K3 (CA). GRIEBEL, Philip [CA/CA]; Box 36, RR5, Saskatoon, Saskatchewan S7K 3J8 (CA). MUTWIRI, George [CA/CA]; 569 Nordstrum Road, Saskatoon, Saskatchewan S7K 7X6 (CA). HECKER, Rolf [DE/DE]; Benrodestr. 60, 40597 Düsseldorf (DE).

(22) International Filing Date:

19 September 2003 (19.09.2003)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

60/412,479 19 September 2002 (19.09.2002) US

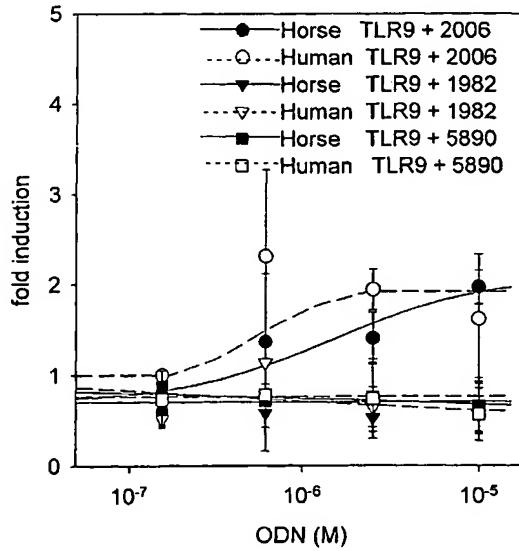
(74) Agent: STEELE, Alan, W.; Wolf, Greenfield & Sacks, P.C., 600 Atlantic Avenue, Boston, MA 02210 (US).

(71) Applicants (for all designated States except US): COLEY PHARMACEUTICAL GMBH [DE/DE]; Elisabeth-Selbert-Strasse 9, 40764 Langenfeld (DE). UNIVERSITY OF SASKATCHEWAN [CA/CA]; Kirk Hall, 117 Science Place, Saskatoon, Saskatchewan S7N 5C8 (CA). QIAGEN GMBH [DE/DE]; Max-Volmer-Strasse 4, 40724 Hilden (DE).

(81) Designated States (national): AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX,

{Continued on next page}

(54) Title: TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES



WO 2004/026888 A2

(57) Abstract: Novel amino acid and nucleotide sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) Toll-like receptor 9 (TLR9) are provided. Also provided are amino acid and nucleotide sequences for dog (canine), cat (feline), mouse (murine), and human TLR9. Comparison of these sequences, especially in combination with functional assessment for species-specific CpG motif preferences, permits identification of specific regions and amino acid residues of interest in TLR9 ligand interaction. Novel chimeric TLR9 receptor molecules, cells expressing these molecules, and methods for their use in screening assays for TLR9 ligands are also provided.



MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(84) **Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO,

TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES**Background of the Invention**

Synthetic oligodeoxynucleotides (ODN) and DNA containing immunostimulatory CpG motifs (CpG DNA) function as potent adjuvants and activators of the innate immune system. Heeg K et al. (2000) *Int Arch Allergy Immunol* 121:87-97; Krieg AM (2001) *Vaccine* 19:618-22. A wide variety of CpG-containing sequences have been screened for biological activity and it is reported that optimal CpG DNA sequences can vary among species. Rankin R et al. (2001) *Antisense Nucleic Acid Drug Dev* 11:333-40.

Toll-like receptor 9 (TLR9) has recently been identified as a receptor for CpG ODN. Hemmi H et al. (2000) *Nature* 408:740-5. The molecular mechanism by which TLR9 recognizes CpG DNA is not understood.

Summary of the Invention

Toll-like receptor 9 (TLR9) is known to be involved in innate immunity and to signal in response to CpG DNA. To date, the amino acid sequences only of human and murine TLR9 have been reported, and, interestingly, these two species are known to prefer different CpG motifs. The structural basis for this species-specific CpG motif preference has not yet been fully elucidated. The instant invention provides, in part, novel amino acid and nucleotide sequences of rat, pig, cow, and horse TLR9. These novel TLR9 sequences are useful for elucidating certain key structural features of TLR9. Specifically, comparison of sequences of murine, human, and these novel TLR9 sequences permits identification of areas of highly conserved sequence, areas of group conservation, and areas of hypervariability. In addition, such comparisons permit an assessment of evolutionary relatedness among TLR9 molecules of the various species, as well as an assessment of inter-species homologies. Importantly, such comparisons permit a rational basis for identifying amino acids in TLR9 that may be involved in the CpG binding site, as well as amino acids involved in conferring species specificity for particular CpG motifs. Such information may be used to design and construct novel TLR9 molecules which incorporate specific point or regional mutations and which possess desired ligand binding characteristics. Such information may also be useful in designing and identifying novel ligands for TLR9 of a given species.

- 2 -

In one aspect, the invention provides isolated polypeptides having amino acid sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) TLR9 polypeptides. These amino acid sequences correspond to SEQ ID NOs 1, 5, 9, 13, and 17, respectively. Each of these sequences is believed to include at least a majority of an 5 extracellular domain, as well as a transmembrane region and at least part of a TLR/IL-1 receptor (TIR) domain. To the extent any such sequence may lack an amino-terminal and/or carboxy-terminal sequence, such sequence is ascertainable, without undue experimentation, using conventional molecular biology techniques and the sequence information provided herein.

10 In another aspect the invention provides isolated polypeptides having amino acid sequences for essentially the whole extracellular domain, optionally including a signal peptide, of each of rat, porcine, bovine, equine, and ovine TLR9. These amino acid sequences correspond to SEQ ID NOs 2, 6, 10, 14, and 18, respectively. Such extracellular domains are believed to include sequence specifically involved in binding to TLR9 ligand, 15 such as CpG DNA. In addition, such extracellular domains are believed to include sequence that confers species specificity for particular CpG motifs.

Isolated nucleic acid molecules encoding the polypeptides just described above are also provided according to further aspects of the invention. Such nucleic acid molecules include, but are not limited to, nucleic acid molecules having sequences provided by SEQ ID 20 NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively. Isolated nucleic acid molecules encoding the TLR9 polypeptides of SEQ ID NOs 1, 5, 9, 13, 17; and 2, 6, 10, 14, and 18 also include nucleic acid molecules that differ in sequence from SEQ ID NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively, due to degeneracy of the genetic code. Such nucleic acid molecules will hybridize, under stringent conditions, with suitably selected nucleic acid 25 molecules having sequences selected from SEQ ID NOs 3, 4, 7, 8, 11, 12, 15, 16, 19, and 20.

In another aspect the invention provides a vector which includes an isolated nucleic acid molecule of the invention. In one embodiment the vector is an expression vector and the isolated nucleic acid molecule of the invention is operably linked to a regulatory sequence in the vector. When present within a cell, an expression vector according to this aspect of the 30 invention causes the cell to express a polypeptide of the invention.

The invention according to another aspect provides a cell in which a vector of the invention is present. In one embodiment the cell containing the vector expresses a

polypeptide of the invention. In certain embodiments the cell also contains a reporter construct that transduces a TLR9-mediated signal in response to contact of the polypeptide of the invention or a TLR9 with a suitable TLR9 ligand. The cell containing the vector, and optionally containing the reporter construct, can be used in screening methods also provided by the invention.

In yet another aspect the invention provides an antibody or antibody fragment that binds specifically to an isolated polypeptide of the invention. In certain embodiments the antibody or antibody fragment binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide. More specifically, the antibody or antibody fragment binds uniquely to one of the isolated polypeptides of the invention. In one embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide also binds to either mouse or human TLR9. In another embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide does not also bind to either mouse or human TLR9. In some embodiments the antibody or antibody fragment binds selectively to a chimeric TLR9 polypeptide of the invention. In certain embodiments the antibody or antibody fragment of the invention is a monoclonal antibody or fragment of a monoclonal antibody.

In one aspect the invention provides a method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the first species. The method involves aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species; generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

In another aspect the invention provides a method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9. The method according to this aspect of the invention involves aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a CpG DNA optimized for murine TLR9; generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids. In one embodiment the method according to this aspect of the invention is performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred CpG DNA).

In another aspect the invention also provides an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (extracellular domain (ECD) of murine TLR9) except for substitution of at least one key amino acid identified according to the method above. The polypeptide according to this aspect of the invention is a chimeric TLR9 polypeptide. Preferably the polypeptide according to this aspect of the invention binds to CpG DNA optimized for human TLR9 better than does the isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (ECD of murine TLR9). In one embodiment the polypeptide includes only one substituted amino acid. The isolated polypeptide according to this aspect of the invention may further include sequence involved in TLR/IL-1R signal transduction, e.g., intracellular domain of TLR9 as provided in SEQ ID NOs 29 and 33. For example, in one embodiment a polypeptide according to this aspect of the invention is an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:29 (full length murine TLR9) except for substitution of at least one key amino acid identified according to the method above.

In another aspect the invention provides an isolated nucleic acid molecule including a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described. In one embodiment the isolated nucleic acid molecule has a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described.

5 In yet another aspect, the invention provides a screening method to identify a TLR9 ligand. The method involves contacting a polypeptide (including a chimeric TLR9 polypeptide) of the invention with a candidate TLR9 ligand; measuring a signal in response to the contacting; and identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling. In one embodiment 10 the candidate TLR9 ligand is an immunostimulatory nucleic acid. In one embodiment the candidate TLR9 ligand is a CpG DNA.

The invention also provides, in yet a further aspect, a screening method to identify species-specific CpG-motif preference of an isolated polypeptide of the invention. The method according to this aspect of the invention involves contacting an isolated polypeptide 15 of the invention with a CpG DNA including a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG; measuring a signal in response to the contacting; and identifying a species-specific CpG-motif preference when the signal in 20 response to the contacting is consistent with TLR9 signaling. In one embodiment the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

	TCCATGACGTTTGATGTT	(SEQ ID NO:39),
	TCCATAACGTTTGATGTT	(SEQ ID NO:40),
	TCCATCACGTTTGATGTT	(SEQ ID NO:41),
25	TCCATTACGTTTGATGTT	(SEQ ID NO:42),
	TCCATGGCGTTTGATGTT	(SEQ ID NO:43),
	TCCATGCCGTTTGATGTT	(SEQ ID NO:44),
	TCCATGTCGTTTGATGTT	(SEQ ID NO:45),
	TCCATGATGTTTGATGTT	(SEQ ID NO:46),
30	TCCATGAAGTTTGATGTT	(SEQ ID NO:47),
	TCCATGAGGTTTGATGTT	(SEQ ID NO:48),
	TCCATGACATTTGATGTT	(SEQ ID NO:49),
	TCCATGACCTTTGATGTT	(SEQ ID NO:50),
35	TCCATGACTTTGATGTT	(SEQ ID NO:51),
	TCCATGACGTTTGATGTT	(SEQ ID NO:52),
	TCCATGACGATTTGATGTT	(SEQ ID NO:53),
	TCCATGACGGTTTGATGTT	(SEQ ID NO:54),

- 6 -

TCCATGACGTCTTGATGTT (SEQ ID NO:55),
TCCATGACGTATTGATGTT (SEQ ID NO:56), and
TCCATGACGTGTTGATGTT (SEQ ID NO:57).

In certain embodiments of the screening methods of the invention, the signal includes
5 expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway. In one embodiment the reporter gene is operatively linked to a promoter sensitive to NF- κ B. In one embodiment the signal in response to contacting is binding of the candidate TLR9 ligand or CpG DNA to the polypeptide of the invention.

In one embodiment the screening method is performed on a plurality of test
10 compounds. In one embodiment the response mediated by the TLR9 signal transduction pathway is measured quantitatively and the response mediated by the TLR9 signal transduction pathway associated with each of the plurality of test compounds is compared with a response arising as a result of an interaction between the functional TLR9 and a reference immunostimulatory compound.

15

Brief Description of the Figures

Figure 1 depicts a Clustal W multiple sequence alignment of deduced amino acid sequences for cat (feline), dog (canine), cow (bovine), mouse (murine), sheep (ovine), pig (porcine), horse (equine), human, and rat TLR9 polypeptides. The deduced amino acid
20 sequences for feline, canine, bovine, murine, ovine, porcine, equine, human, and rat TLR9 polypeptides shown in the figure correspond to SEQ ID NOs 25, 21, 9, 29, 17, 5, 13, 33, and 1, respectively. Lines labeled "multiple" refer to the multiple sequence alignment of all six sequences shown. Lines labeled "mo/hu" refer to a paired sequence alignment of mouse and human TLR9 sequences alone.

25 Figure 2 is a cladogram depicting an evolutionary relatedness tree for rat, murine, porcine, bovine, equine, and human TLR9 polypeptides in Figure 1.

Figure 3 is a graph depicting species specificity of TLR9 signaling with selected oligonucleotides having strong specificity for human (2006), mouse (5890), or neither (1982).

30

Detailed Description of the Invention

The present invention provides novel amino acid and nucleotide sequences for TLR9 derived from rat, pig, cow, horse, and sheep. These sequences can be used to identify key features of the primary sequences of these and related TLR molecules, including previously

known primary sequences of human and mouse (murine) TLR9. Such key features include binding site information and species specificity toward particular CpG motifs. Native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to identify and to design novel TLR9 ligands.

5 Additionally, the native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to compare various TLR9 ligands, including CpG DNA.

In one aspect the invention provides isolated TLR9 polypeptides, and isolated nucleic acid molecules encoding them, from rat, pig, cow, horse, and sheep. The term "isolated" as used herein with reference to a nucleic acid molecule or polypeptide means substantially free of or separated from components with which it is normally associated in nature, e.g., other nucleic acids, proteins, lipids, carbohydrates or *in vivo* systems to an extent practical and appropriate for its intended use. In particular, the nucleic acids or polypeptides are sufficiently pure and are sufficiently free from other biological constituents of host cells so as to be useful in, for example, producing pharmaceutical preparations. Because an isolated nucleic acid or polypeptide of the invention may be admixed with a pharmaceutically acceptable carrier in a pharmaceutical preparation, the nucleic acid or polypeptide may represent only a small percentage by weight of such a preparation. The nucleic acid or polypeptide is nonetheless substantially pure in that it has been substantially separated from the substances with which it may be associated in living systems.

An amino acid sequence of rat TLR9 is provided as SEQ ID NO:1. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:1 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of rat TLR9 (See 25 Figure 1). Amino acids numbered 1-821 of SEQ ID NO:1 are presumptively extracellular domain and correspond to SEQ ID NO:2. SEQ ID NO:3 is a nucleotide sequence of rat TLR9 cDNA having an open reading frame corresponding to nucleotides 1-3096. SEQ ID NO:4 is a nucleotide sequence of rat cDNA encoding amino acids 1-821 of SEQ ID NO:1.

An amino acid sequence of porcine TLR9 is provided as SEQ ID NO:5. Based on 30 comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:5 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of porcine TLR9

- 8 -

(See Figure 1). Amino acids numbered 1-819 of SEQ ID NO:5 are presumptively extracellular domain and correspond to SEQ ID NO:6. SEQ ID NO:7 is a nucleotide sequence of porcine TLR9 cDNA having an open reading frame corresponding to nucleotides 77-3166. SEQ ID NO:8 is a nucleotide sequence of porcine cDNA encoding amino acids 1-819 of SEQ ID NO:5.

An amino acid sequence of bovine TLR9 is provided as SEQ ID NO:9. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:9 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of bovine TLR9

10 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:9 are presumptively extracellular domain and correspond to SEQ ID NO:10. SEQ ID NO:11 is a nucleotide sequence of bovine TLR9 cDNA having an open reading frame corresponding to nucleotides 84-3170. SEQ ID NO:12 is a nucleotide sequence of bovine cDNA encoding amino acids 1-818 of SEQ ID NO:9.

15 An amino acid sequence of equine TLR9 is provided as SEQ ID NO:13. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:13 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of equine TLR9

(See Figure 1). Amino acids numbered 1-820 of SEQ ID NO:13 are presumptively extracellular domain and correspond to SEQ ID NO:14. SEQ ID NO:15 is a nucleotide sequence of equine TLR9 cDNA having an open reading frame corresponding to nucleotides 115-3207. SEQ ID NO:16 is a nucleotide sequence of equine cDNA encoding amino acids 1-820 of SEQ ID NO:13.

An amino acid sequence of ovine TLR9 is provided as SEQ ID NO:17. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:17 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of ovine TLR9 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:17 are presumptively extracellular domain and correspond to SEQ ID NO:18. SEQ ID NO:19 is a nucleotide sequence of ovine TLR9 cDNA having an open reading frame corresponding to nucleotides 92-3178. SEQ ID NO:20 is a nucleotide sequence of ovine cDNA encoding amino acids 1-818 of SEQ ID NO:17.

SEQ ID NO:1 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAELALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAEPRSNITSLSLIANRI
 5 HHLHNLDVFVLPNVRQLNLKWCNCPPGLSPLHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL
 SHTNILVLDASSLAGLHSLRVLFMMDGNCCYKNPCNGAVNVTPDAFLGLSNLTHLSLKYNNLTEVPRQLPPSLEYL
 LLSYNNLIVKLGAEIDLNLTSRMLDVGGNCRRCDHAPDLCTECRQKSLLDHQPTFHHLSHLEGVLKDSSLHSLN
 SKWFQGLANLSVLDLSENFLYESINKTSAFQNLTRLRLDLSFNYCKKVFSARLHLASSFKSLVSLQELNMNGIF
 FRLLNKNTLRLWLAGLPKLHHTLHQMFNINQAOQLSVFSTFRALRFVDSLNNRISGPPTLSRVAPEKADEAKGVPW
 10 PASLTPALPSTPVSKNFMVRCKNLRFTMDLSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK
 VLDLSYNKLDLYHSKSFSelpQQLQALDLSYNSQPFMSMQGIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYSTS
 VEYLDGNGVGVRMWDEEDLYLYFFQDLRSLIHLDLSQNLHILRPQNLNYLPKSLSRKLSFRDNHLSFFNWSSL
 15 FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVPAFFALAVELKEVNLSHNLKTVDRSWFGPIV
 MNLTVDVSSNPLHCACGAPFVDLLLEVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFGLSLL
 AVAVGTVLPPLLQHLCGWDVWYCFHLCALWPLLTRGRRSAQALPYDAFVVFDAKAQSAVADWVYNELRVLEERRG
 15 RRALRLCLEDRDWLPGQTLFENLWASIYGRKTLFVLAHTDKVSGLLRTSFLLAQQLLEDRKDVVVLVILRPDA
 HRSRYVRLRQRLCRQSVLFWPQNGQGSFWAQLSTALTRDNHHFYNRNFCRGPTAE

SEQ ID NO:2 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAELALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAEPRSNITSLSLIANRI
 20 HHLHNLDVFVLPNVRQLNLKWCNCPPGLSPLHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL
 SHTNILVLDASSLAGLHSLRVLFMMDGNCCYKNPCNGAVNVTPDAFLGLSNLTHLSLKYNNLTEVPRQLPPSLEYL
 LLSYNNLIVKLGAEIDLNLTSRMLDVGGNCRRCDHAPDLCTECRQKSLLDHQPTFHHLSHLEGVLKDSSLHSLN
 SKWFQGLANLSVLDLSENFLYESINKTSAFQNLTRLRLDLSFNYCKKVFSARLHLASSFKSLVSLQELNMNGIF
 FRLLNKNTLRLWLAGLPKLHHTLHQMFNINQAOQLSVFSTFRALRFVDSLNNRISGPPTLSRVAPEKADEAKGVPW
 25 PASLTPALPSTPVSKNFMVRCKNLRFTMDLSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK
 VLDLSYNKLDLYHSKSFSelpQQLQALDLSYNSQPFMSMQGIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYSTS
 VEYLDGNGVGVRMWDEEDLYLYFFQDLRSLIHLDLSQNLHILRPQNLNYLPKSLSRKLSFRDNHLSFFNWSSL
 30 FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVPAFFALAVELKEVNLSHNLKTVDRSWFGPIV
 MNLTVDVSSNPLHCACGAPFVDLLLEVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFG
 30

SEQ ID NO:3 (Rat TLR9)

atgggtctctgtcgaggacccctgcaccccttgtctctcctggtagacggccgcagtgcggctgaggctctggcc
 35 ctgggtaccctgcctgccttctaccctgtgaactgaaggctcatggcctggtagactgcactggcttccct
 aagtctgtgcctcacttctctgcccgcagaaccccgttccaacatcaccagccttcctgtatgcaccaaccgcac
 caccacctgcacaacccctgcactttgtccacccctgccaacgtgcacagctgaacctcaactgtggactgtccgc
 40 cccctgcactgcacttctccctgcacttctccctgcgcatgaccattgagccaaaaccttccctggctatgcgc
 gaagagctgaacctgagctataacggatcaccactgtgccccccctgcccagctccctgacgaactctgagcc
 agccacaccaacatcctggactcgatgccagcgcctcgctggcactgcacagcctgcgagttcttccatggac
 gggactgtactacaagaacccctgcaacggggcggtgaacgtgaccccgacgccttccctgggttggac
 45 ctcacccacttgccttaagtataacaacctcacaagggtgcggccactgcctggggacttgc
 ctgctgcctataacctcatcgtaagctggggccgaagacccctagccaaacctgcaccccttgcata
 gtgggtggaaattggcgcgtgtatcaccgcggccactctgtacagaatgcggcagaagtcccttgc
 caccctcagacttccatcacctgagccacccctgtggactgtggacctaagcgagaacttcttac
 tccaaagtgggtccagggtctggcgaacctctcggtgtggacctaagcgagaacttcttac
 50 aaaacccaggcccttcagaaacctgacccgtctgcgcacactgcacccctgc
 ttgcggccctccacctggcgaagttcctcaagaggctggctgtgcggactgcacccatcttc
 ttccgcttactcaacaagaacacgcgtcaggctggctgtggactgcacccatcttc
 aatttcatcaaccaggcgcagctcagctgtccatggactgcggccacttgc
 cgcacatcgccggccctccaaacctgtggactgtccatggcggagaagggggttccatgg
 cctgcaagtctcacccctgacttcccgagactcccgacttcaaaaggacttcat
 ttcacccatggacccctgtctcggaacaaccagggtgactatcaaggc
 tgcggactgtccctataacaagctggacccatcgatccatcg
 tgcggactgtccctataacaagctggacccatcgatccatcg
 gtgcggactgtccctataacaagctggacccatcgatccatcg

- 10 -

ctggacacctgagactacaacagccagccattcagcatgcaggggataggccacaacttcagtttctggccaatctg
 tccagggtacagaacaccttagcctggcacacaatgacattcacagccgcgtgcctcacgcctctacagcacctca
 gtggagtatctggacttcagccgcaacgggtgtggccgcattgtggacgaggaggactttaccttatttc
 5 caagacacctgagaagccctgattcatctggacctgtcagaataagctgcacatcctccggccccagaacacctcaac
 taccccccagagccctgacgaagctgagttccgtgacaatcacctcttctttaactggagcagtcgtggcc
 ttccctggccaaatctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcaccctgcctaa
 ggcacgcctccagaaaactggatgtcagtagcaacagttatcgtctttgtggcccccagccttcttgctctggcg
 gtagagctaaaagaggtaacctcagccataacatcctcaagactgtggatgcctcgtgcggcaccctttagtgc
 10 atgaacacctgacggttctagacgtgagcagcaacccctctgcattgtgcctcgtgcggcaccctttagtgc
 ctggaaagtgcagaccaagggcctggcttaacgggtgtgaagtgtggcagtcctccggactgccttggccttcactc
 agcatcttgcgcacgcctgcggctgtgcctggatgcgtccttctcggactgccttggccttcactc
 gctgtggccgtggcggcgggtgtgccttactgcacatctcgcggctggacgtctggactgtttccatctg
 15 tgccctggcatggctaccttgcattgcaccctgtggccggcggcggcggcggcggcggcggcggcggcggcgg
 ttgcataaggcgcagagcgcgggtgtgactgggtgtataacagagcttcgagtgccggctagaggagcggcggcgg
 cgg
 20 cgg
 tccatctatggcagccgcacgcactctgtttgtgcggccacacggacaaggactgcgtggccctcgcgcaccaggc
 ttccctggctcagcgcgcctgcggaggaccgcggcggcggcggcggcggcggcggcggcggcggcggcggcggc
 caccgcgtcccgctacgtgcactgcgcgcacgc
 gggcaggggcagctctggcccaagctgagtagcagccctgacttagggacaaccaccacttataaccggaaactc
 tgccggggacctacagcagaatag

SEQ ID NO:4 (Rat TLR9)

atggttctctgtcgcaggacccctgcaccccttgcacggccgtgttcctctgggtacaggccgcagtgcgtggctgaggctctggcc
 ctgggtaccctgcctgccttctaccctgtgaactgaagccctcatggcctggtagactgcacactggcttcttc
 25 aagtctgtgcctcacttcttcgcgcagaaccccttccaaacatcaccaggccttccttgcattgcacccgcac
 caccacctgcacaaacctcgactttgtgcacccctgcgcacatctccgcgcgcgcgcgcgcgcgcgcgcgc
 cctggcctcagcccttgcacttctccgc
 30 gaagagctgaacctgagctataacgggtatcaccactgtgcggccgcgcgcgcgcgcgcgcgcgcgcgc
 agccacaccaacatcctggactcgatgc
 gggactgactactacaagaacccctgcacgggggggtgaacgcgcgcgcgcgcgcgcgcgcgcgc
 ctcacccacttgccttaagtataacaacacctcacagagggtgcggccactgcgcgcgcgcgcgc
 35 ctgcgtcctataacctcatcgtaagctggggggcgaagacttagccacactgcgcgcgcgcgcgcgc
 gtgggtgggaattgcgtcgctgtgatcagcccccgcacctctgtacagaatgcggcagaagtccttgc
 caccctcagacttccatcacctgagccacccctgaaaggcctgtgcgtgcgcgcgcgcgcgc
 tccaagtggttccagggtctggcgaaccttcggacttcggacttcggacttcggacttc
 40 aaaaacccaggcgcccttcagaacacctgcacccgtctgcgcacgcgcgcgcgcgcgcgc
 ttccggccgcctccacctggcaagttccctcaagagccctgtgcgcgcgcgcgcgc
 ttccgcctactcaacaagaacacgcgcgcgcgcgcgcgcgcgcgcgc
 aatttcatcaaccaggcgccgcgcgcgcgcgcgcgcgcgc
 45 cgcatcaggccgcctccaaacctcgacttcggacttcggacttcggacttc
 cctgcacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc
 ttccaccatggactcttcggacttcggacttcggacttc
 tgcgtcgacttcggacttcggacttcggacttcggacttc
 gtgcgtggacacttcggacttcggacttcggacttc
 50 ctggacacctgagactacaacagccagccattcagcatgcaggggataggccacaacttc
 tccagggtacagaacaccttagcctggcacacaatgacattcacagccgcgtgcctcacgcctctacagcacctca
 gtggagtatctggacttcagccgcaacgggtgtggccgcattgtggacgaggaggactttaccttatttc
 caagacacctgagaagccctgattcatctggacctgtcagaataagctgcacatcctccggccccagaacacctcaac
 taccccccagagccctgacgaagctgagttccgtgacaatcacctcttctttaactggagcagtcgtggcc
 ttccctggccaaatctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcaccctgcctaa
 ggcacgcctccaggaaaactggatgtcagtagcaacagttatcgtcttgcggcccttcatttgccttc
 55 gttagagctaaaagaggtaacctcagccataacatcctcaagactgtggatgcgcgcgcgcgcgc
 atgaacacctgacggttctagacgtgagcagcaacccctctgcattgtgcctgcggcgcaccctttagacttactg
 ctggaaagtgcagaccaagggcctggcattgcggcattgcggcattgcggactgccttgcggactgc
 agcatcttgcgcacgcctgcggctgtgcctggatgcgtccttcgcggactgccttggc

- 11 -

SEQ ID NO:5 (Porcine TLR9)

5 MGPRTCLHPLSLLVQVTALAAALAQGRLP AFLP C E L Q P H G L V N C N W L F L K S V P H F S A A P R A N V T S L S L L S N R I H
H L H D S D F V H L S S L R T L N L K W N C P P A G L S P M H F P C H M T I E P N T F L A V P T L E E L N L S Y N S I T T V P A L P D S L V S L S L S
R T N I L V L D P T H T L G L H A L R Y L Y M D G N C Y Y K N P C Q G A L E V V P G A L L G L G N L T H L S L K Y N N L T E V P R S L P P S L E T L L
L S Y N H I V T L T P E D L A N L T A L R V L D V G G N C R R C D H A R N P C R E C P K D H P K L H S D T F S H S R L E G L V L K D S S L Y N L D T
R W F R G L D R L Q V L D L S E N F L Y D C I T K T T A F Q G L A R L R S L N L S F N Y H K K V S F A H L H L A P S F G H L R S L K E L D M H G I F F
R S L S E T T L Q P L V Q L P M L Q T L R L Q M N F I N Q A Q L S I F G A F P G L L Y V D L S D N R I S G A A R P V A I T R E V D G R E R V W L P S R
N L A P R P L D T L R S E D F M P N C K A F S F T I D L S R N N L V T I Q S E M F A R L S R L E C L R L S H N S I S Q A V N G S Q F V P L T S L R V L
D L S H N K L D L Y H G R S F T E L P R L E A L D L S Y N S Q P F T M Q G V G H N L S F V A Q L P A L R Y L S L A H N D I H S R V S Q Q L C S A S L C
10 A L D F S G N D L S R M W A E G D L Y L R F F Q G L R S L V W L D L S Q N H L H T L L P R A L D N L P K S L K H L H L R D N N L A F F N W S S T L L L
P K L E T L D L A G N Q N K A L S N G S L P S G T Q L R R L D L S G N S I G F V N P G F F A L A K Q L E E L N L S A N A L K T V E P S W F G S M V G N
L K V L D V S A N P L H C A C G A T F V G F L L E V Q A A V P G L P S R V K C G S P G Q L Q G H S I F A Q D L R L C L D E T L S W N C F G I S I L L A M
A L C L V V P M L H H L C G W D L W Y C F H L C L A W L P H R G Q R R G A D A L F Y D A F V V F D K A Q S A V A D W V Y N E L R V Q L E E R R G R A
15 L R L C L E E R D W L P G K T L F E N L W A S V Y S S R K T L F V L A H T D R V S G L L R A S F L L A Q Q R L L E D R K D V V V L V I L R P D A Y R S
R Y V R L R O R L C R O S V L L W P H O P R G Q G S F W A Q L G T A L T R D N H H F Y N R N F C R G P T T A E

SEQ ID NO:6 (Porcine TLR9)

20 MGPRLCTLHPLSLLVQVTALAAALAQGRLPAFLPCELOPHGLVNCNWLFLKSVPFHSAAPRANVTSLSLLSNRIH
HLHDSDFVHLSSLRTLNWKNCPPAGLSPMHFPCHMTIEPNFTFLAVPTLEELNSYNSTITVPALPDSLVSLSLS
RTNILVLDPTHLTGLHALRYLYMDGNCYYKNPQCQALEVVPGALLGLGNLTHLSLKYNNLTEVPRSLPPSLETLL
LSYNHIVTLPEDLANLTALRVLDDVGGNCRRCDHARNPCRECPKDHPK1LHSDFTSHLSRLEGVLKDSSLYNLDT
RWFRLGLDRLQVLDLSENFLYDCITKTTAFQGLARLRLSLSNLSFNYHKKVSFAHLHLAPSFGHLRSLKEELDMHGIFF
RSILSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLYVDLSDNRISGAARPVAITREVGDGRERVWLPSR
25 NLAPRPLDTRLSEDFFMPNCKAFSFTLDSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTLSLRVL
DLSHNKLDLYHGRSFTELPRLEALDLISYNSQPFTM0QVGHNLSFVAOLPALRVLSLAHNDIHSRVSQQLCSASLC
ALDFSGNDLSSRMWAEGDLYLRLFFQGLRSLVWLDLSQNHHLHTLLPRA LDNLPKS LKHLHRLDNNLIAFFNWSSLTLL
PKLETLDLAGNQLKALNSGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSMVGN
LKVLDDVSANPLHACGATEFGFLLVEVOAAVPGPLPSRVKCGSPGOLOGHSIFAODRLCLDETLSWNCFG

30 SEQ ID NO:7 (Porcine TLR9)

35 gagcacgaacatccctactgttagctgctgcccggctgcagccagacccttggagaagaccccactccctgt
catggggcccccgctgcacccctgcacccctttctctctgggtgcaggtgacagcgcggctgcggctctggccca
gggcaggctgcctgcctccctgtgagctccagccccacggcctggtaactgcaactggctttctctgaa
gtccgtccccacttctcgccggcagcgcggccggcaacgtcaccagccctccctactctccaacccgatcca
ccacctgcacgactccgacttcgtccacctgtccagcctacgaactctaaccctaagtgaaactgcccggcggc
tggcctcagccccatgcacttccctgccacatgaccatcggccaaacacccttctggccgtgcccaccctggaa
ggagctgaacctgagctacaacagcatcaccgcggcggccactccctgtgtccctgtcgtgag
ccgcaccaacatccctgggtctagaccccacccacccactggcctacatgcccctgcgtacccgtacatggatgg
caactgctactacaagaacccctgcacggggggcgtggagggtggtgccgggtgcccctccctggccctggcaaccc
40 cacacatctctcactcaactacaagaacccctgcacggggggcgtggagggtggtgccgggtgcccctccctggccctggcaaccc
gttgcctacaaccacattgtcacccctgacgcgtgaggactggccaaatctgactgcctgcgcgtgttgcgt
gggggggaactgcccggcgtgtgaccatgcccgaacccctgcacgggagtgcccuaaggaccaccccaagctgca
ctctgacacccctcagccacccctgagccgcctcgaaggcctggttgaaagacagttctcttacaacccctggacac
45 cagggtggttccgaggcctggacaggctccaaagtgtggactgtgagaacttctctacgactgcaccc
gaccacggccctccagggcctggccgactgcgcagccctaaaccctgtccctcaattaccacaagaagggtgcctt
tgccccacccctgcacccctggccacccctcccttgggcacccctccggccctgaaaggagctggacatgcaccc
ccgctcgctcaagtggagaccacgcgtccaaaccctctggccaaactgcctatgctccagaccctgcgcctgcagatgaa
50 cttcattaaaccaggcccaagctcagcatcttggggccctccctggccctgtacgtggacccatcgaccc
catcagcggagactgcaaggccagggtggcattactaggagggatggtagggagagggtctggctgcctccag
gaacccctgcctccacgtccactggacactctccgcctcagaggacttcatgccaactgcaaggccctcagcc
cttggacccctgtctcggaacaaccctgggtgacaatccaggactggagatgtttgtcgccctcgcgcctcgagtgcc
gcccgcgtggccacaacacgcacatctcccgaggcggtaatggctctcagttgtccgcgtgaccagccctgcgggtgt
ggacccctgtcccaacaacaagctggacccctgtatcacgggcgtcgttgcacggagactggccgcctggaaagactgg
cctcagctacaatagccaccccttaccatgcagggtgtggccacaacccctcagccctgtggcccaagctgcggcc

- 12 -

SEQ ID NO:8 (Porcine TLR9)

25 atggggcccccgctgcaccctgcacccctttctctcctggtgaggtacagcgctggctggccatggcc
ggcaggctgcctgccttcctgcctgtgagctcagccccacggcctggtaactgcaactgctcttcga
tcctgccttcacttctccggcggcagcggccacgtcaccagcctctccttactctccaaccgcattcac
cacctgcacgactccgacttcgtcaccctgtcagcctacgaactctcaacctcaagtggactgcccgg
ggcctcagccccatgcacttccctgcccacatgaccatcgagccaaacaccccttcggcgtcccaccctgg
gagctgaacctgagctacaacagcatcagcaccgtgcctgcccactccctgtgtccctgtcgctgagc
cgccaccaacatcctgggtctagaccccccacccacactggcctacatgcccctgcgtacctgtacatggatgg
aactgtactacaagaacccctgcccaggggcgtggagggtgggtgcccgggtcccttctcgccctggcaaccc
acacatctctcactcaagtacaacaatctcagggagggtcccccgccctgccccccagcctggagaccctgctg
ttgtcctacaaccacattgtcaccctgacgcctgaggacctggcaatctgactgcccctgcgtgttatgt
ggggggaaactgcccggctgtgaccatgcccgaacccctgcagggagtgcccaaaaggaccacccaaagctgcac
tctgacacccctagccacctgagccgcctgcgaaggcctgggttgaagacagttctctacaacctggacacc
agggtgttcccgaggccctggacaggctcaagtgtggacactgagtgagaacttccctctacgactgcaccaag
accacggcctccaggggctggcccgactgcgcagcctcaacctgtcctcaattaccacaagaagggtgtcc
gcccacctgcacctggcaccctccttggcacctccggccctgaaggagctggacatgcacatggcatcttc
cgctcgctcagtgagaccacgcgtcaacactctggtccaactgcctatgtccagaccctgcgcctgcagatgaac
40 ttccattaaccaggcccagctcagcatcttgggccttcctggcctgtgtacgtggacccatcgaccaaccgc
atcagcggagctgcaaggccagtgccattactagggagggtggtagggagagggtctggctgccttcagg
aacctcgctccacgtccactggacactctccgctcagaggacttcatgccaaactgcacaggccctcagcttcacc
ttggacctgtctcggaaacaacctggtacaatccagtcggagatgttgcctcctcaccgcctcgagtgcc
cgccctgagccacaacacgcattcccaaggccgtcaatggctctcagttgtccgtgaccaggcctgcgggtgctg
45 gacctgtcccacaacaagctggacctgtatcacggcgcgttcacggagctggcgcctggaaagcactggac
ctcagctacaatagccagcccttaccatgcaggggtggccacaacctcagctcgtggcccgactgcggcc
ctgcgtacccatcagcctggcgcacaatgcacccatagccagtgccagcgcgtctgttagcgcctcactgtgc
gccctggactttagccggaaacgcattgcagccggatgtgggctgagggagacccatctccgttccaaaggc
ctaagaaggcttagctggctggacctgtcccagaaccacccatgcacacccttcgtccacgtgcctggacaaccc
50 cccaaaaggctgaagcatctgcacatccgtgacaataaccctggccttcactggagcgcgcctgaccctcctg
cccaagctggaaaccctggacttggctggaaaccacgcattgcagggcctaaagcaatggcagcgcctgaccctcctg
cagctgcggaggctggacccatcagtgccaaacgcattgcagggccttgcgttgcaccctggccaaaggc
tttagaagagctcaaccctcagcgcctcaagacactgtggagcccttcgtgttggctcgatggggcaac
ctgaaaaggcttagacgtgagcgccttcgtcactgtgcctgtgggctgacccatcgtggcccttcgtgg
gtacaggctgcgtgcctggctgcccagccgcgtcaagtgtggcagtcggggcagctccaggccatagcatt
55 tttgcgcagacactgcggcttcgtccctggatgagacccttcgtggactgtttttqqc

SEQ ID NO:9 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLPAFLPCELQPHGQVDCNWLFLKSVPHFSAAGAPRANVTSLSLISNRIH
 5 HLHDSDFVHLSNLRVNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSL
 HTSILVLGPTHFTGLHALRFLYMDGNCYYMNPCPRALEVAPGALLGLGNLTHLSLKYNNLTEVPRRLPPSLDTLL
 LSYNHIVTLPAPEDLANLTALRVLVDVGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSSLKLEK
 DWFRGLGRLQVLDLSENFLYDIFTKTTIFMDLTQLRRLNLSFNYHKKVSFAHLHASSFGSLVSLEKLDMHGIFT
 RSLTNITLQSLTRLPKLQSLHLQLNFINQAOQLSIFGAFPSLFLVDLSNDRISGAATPAAALGEVDSRVEVWRLPR
 GLAPGPLDAVSSKDFMPSCNLFNFTLDSLRSNNLVTIQQEMFTRSLQCLRLSHNSISQAVNGSQFVPLTSRLVLD
 10 LSHNKLDLYHGRSFTELPQLEALDLSYNSQPFMGSQVGHNLSFVAQLPSLRLYLSLAHNGIHSRVSQKLSSASLRA
 LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQQLDLSNENHLHTLLPRHLDNLPKSLRQLRLRDNNLAFNWSLTVLP
 RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIPGFFVRATRLELNLSANALKTVDPSWFGSLAGTL
 KILDVSANPLHACGAAVFDFLLERQEAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSDLCFGSLLLMVA
 LGLAVPMLHHLCGWDLWYCFHLCLAHLPRRRQRGEDTLLYDAVVFDKVQSAADVWVYELRVQLEERRGRAL
 15 RLCLEERDWLPKGKTLFENLWASVYSSRKTMFVLDHDRVSGLLRASFLLAQQLLEDRKDVVVLVILRPAAYRSR
 YVRLRQRLCRQSVLLWPHQPSGQGSFWANLGIALTRDNRHFYNRNFCRGPTTAE

SEQ ID NO:10 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLPAFLPCELQPHGQVDCNWLFLKSVPHFSAAGAPRANVTSLSLISNRIH
 20 HLHDSDFVHLSNLRVNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSL
 HTSILVLGPTHFTGLHALRFLYMDGNCYYMNPCPRALEVAPGALLGLGNLTHLSLKYNNLTEVPRRLPPSLDTLL
 LSYNHIVTLPAPEDLANLTALRVLVDVGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSSLKLEK
 DWFRGLGRLQVLDLSENFLYDIFTKTTIFMDLTQLRRLNLSFNYHKKVSFAHLHASSFGSLVSLEKLDMHGIFT
 RSLTNITLQSLTRLPKLQSLHLQLNFINQAOQLSIFGAFPSLFLVDLSNDRISGAATPAAALGEVDSRVEVWRLPR
 GLAPGPLDAVSSKDFMPSCNLFNFTLDSLRSNNLVTIQQEMFTRSLQCLRLSHNSISQAVNGSQFVPLTSRLVLD
 25 LSHNKLDLYHGRSFTELPQLEALDLSYNSQPFMGSQVGHNLSFVAQLPSLRLYLSLAHNGIHSRVSQKLSSASLRA
 LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQQLDLSNENHLHTLLPRHLDNLPKSLRQLRLRDNNLAFNWSLTVLP
 RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIPGFFVRATRLELNLSANALKTVDPSWFGSLAGTL
 KILDVSANPLHACGAAVFDFLLERQEAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSDLCFG
 30

SEQ ID NO:11 (Bovine TLR9)

gggaaagtgggcgccaagcatcctccctgcagctgcctcccaacctgcccggccagaccctctggagaagccgcat
 tccctgtcatggcccccactgtgccccgcacccccccttctctccctgtcagggccggccactggcagccggccc
 tggccgagggcacccctgcctgcctccctgtgagctccagcccatggtcaggtggactgcactggctgt
 35 tcctgaagtctgtgccgactttcggtggagccccccggccaatgtcaccagccctcccttaatctccaacc
 gcatccaccactgtcatgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtggactgcc
 cgccggccgcctcagcccatgacttccctgcgtatgaccatcgagccaaacacccctctgtgtgc
 ccctggaggagctgaacctgagctacaacggcatcaccgaccgtgcctgcctgcggcagttccctgtgtccctgt
 cgctgagccacaccagcatccctgggtctaggccccacccacttcaccggcctgcacccctgcgttccctgtaca
 40 tggacggcaactgtactacatgaaccctgcccggggccctggaggtggcccccaggccctctccggcctgg
 gcaacctcactgcacccgtcgtcaagtacaacaacctcacggagggtggcccccggcctgcggccaggcctggaca
 ccctgtctgtccataaccacattgtcaccctggcaccatggccaaacctgtactgcctgcgtgc
 ttgacgtgggtggaaactggccgctgcaccatggcccaacccctgcagggagggtggccaaaggaaacttccca
 agctgaccctgacaccccttcactgtcaccctgagccgctcgaaggccctgggttgaaggacagttctcttaca
 45 tagagaaagattgggtccggccctggggcaggctcaactgtcaccctgaggttgcacttccttatgactaca
 tcaccaagaccacccatcttcaacccatcacgaccctgactgcgcagactcaacctgtcctcaattaccacaagg
 tgccttcgtccctccctcaccacatcacgctccactgtcaccctgggggacttcccgaggcctgtcttgcaccc
 agctgaacttcatcaaccaggcccagctcagcatcttggggccctggggagggtggacagcagggtggaaacttcc
 50 acaaccgcacgcggagccgcacgcggccacccctggggagggtggacagcagggtggaaacttcc
 tgcccaaggggccctgcgtccaggcccgtggacgcggcgtcagtcacccatccatgcacccatgcaccc
 tcacccatggacccatgtcaccggacaaacctgggtacaatccagcaagagatgtttaccgcctctcc
 gcctgcgcctgagccacaacagcatctgcgcaggcgttaatggctcccgatgcaccgcctgcgg

- 14 -

5 tgctcgaccctgtcccacaacaagctggacctgtaccatggcgctcattcacggagctgccgcagctggaggcac
tgacactagctacaacagccagccctcagcatgcagggcgccccacaacccatcgcttcgtggcccgactgc
cctccctgcgtcacctcagcctgcgcacaatggcatccacagccgcgtgtcacaagaagctcagcagcgcctcg
tgcgccctggacttcagcggcaactccctgagccagatgtggggccagggagacacttatctgtctttca
aaggcttggaggaacctgtccagctggacctgtccgagaaccatctgcacaccctctgcctcgcacctggaca
acctgcccaagagcctgcccagctgcgttcctgggacaataacctggccttcaactggagcagcctgaccg
tcctgccccggcttggaaagccctggatctggcagggaaaccagactgaaggccctgagcaacggcagcctgcccctg
gcatccggctccagaagctggacgtgagcagcaacagcatggcttcgtatcccccgttctcgccgcgca
ctcggtgatagagcttaacctcagcggcaatggccatggatccctctggttcggttccttagcag
ggaccctgaaaatcctagacgtgagcggcaaccggctccactgcgcctgcggggggcccttggacttcctgc
tggagagacaggaggccgtccccggctgtccaggcgcgtcacatgtggcagtcggggccagctccaggggccga
gcatcttcacacaggacccgtgcctctgcctggatgagacccttccttggactgtttggcctctactgctaa
tggtggcgctggccctggcagtgccatgtgcaccacccctgtggctggacccctgttactgttccacactgt
gtctggcccatggcccgacggcgccggcagggggcgaggacaccctgtctatgatgcgcgtgtggcttc
15 acaagggtgcagagtgcagtggctgatgggtgtacaacgcgactccgcgtgcagctggaggagcgcggggggcc
ggcgctccgcctctgcctggaggagcgcgagactggctccctggtaagacgccttcgcagaaactgtgggccteg
tctacagcagccgcagaccatgttcgtgtggaccacacggaccgggtcagcggccctctgcgcgcagctcc
tgcggcccgacgcgcctgtggaggaccgcaggacgcgttagtgcgtgtatgcgccttcgcgcctatc
ggtcccgctacgtgcgggtgcgcgccttcgcgcaggcgtccctctggccccaccagcccgatggcc
20 agggtagttctggccaaacctggcatgcgcctgaccaggacaacgcgtcacttctataacccggaaacttcgc
ggggcccccacgcacagccgaatagcacaaggactgtggccag

SEQ ID NO:12 (Bovine TLR9)

25 atggggcccctactgtgccccgcacccccccttctctccctggcaggcggcggactggcagcggccctggccagg
ggcacccctgcctgccttcgtggactcagccccatggtcaggactgcaactggctgttccctgtaa
tctgtccgcactttcgctggagccccccggccatgtcaccagccctctcttaatctccaaccgcaccc
cacttgcacactctgacttcgtccacccgtccacccgtcaacctcgggtcctcaacctcaagtggaaactggccggcc
ggcctcagccccatgcacttccctgcccgtatgaccatcggccaaacacccctccctggctgtcccccaccctggag
gagctgaacctgagctacaacggcatcagcaccgtgcctgcctgcctgcctgcctgcctgcctgcctgcctgg
30 cacaccagcatcctgggtctaggccccaccacttcacccggcctgcacgcctgcgccttcgtacatggacggc
aactgtctactacatgaacccctgcccggggccctggaggtggcccccaggcgcctccctggccctggcaaccc
acgcacccgtgcgtcaagtacaacaacccatcagcgggtgcctgcctgcctgcctggacaccctgtct
ctgtcttacaaccacattgtcaccctggcaccggaggacctgtactgcctgcgtgctgacgtg
ggtgggaaactggccgcgtgcgaccatgcccgaacccctgcaggagtgcccaaagaacttcccaagctgcac
35 cctgcacacccctcagtcacccgtggccctgcgacggcacttgcgttgcggacacttgcgttgcacccatc
gattgggtcccgccgtggcaggctcaagtgcgtcgcacccgtggagacttcccttatgactacatc
accaccatctcaacgcacctgcaccctgcgacactcaacccatgcctcaattaccacaagaagggtgc
gcctgcacccatcagcgttcccttggagttctgggtgtccctggagaagctggacatgcacggcatcttc
cgctccctcaccacatcagcgtccagtcgtgaccggcgtcccaagctccagactgcacccatc
40 ttcatcaacccaggcccagctcagcatcttggggcctcccgagcctgtcttcgtggacccgtgcggacaaccgc
atcagcggaggccgcacccgcagccagccggccctggggaggtggacaggcagggtggaaacttgc
ggcctcgtcaggcccgtggacccgtcagtcacccatgcacccatgcacccatgcacccatgc
gacctgtcacccatgcacccatgcacccatgcacccatgcacccatgcacccatgcacccatgc
45 ctgagccacaacccatcagcgtcccggttaatggctccctggacttcgtggccgtgaccaggcctgc
ctggacttcggcacaactccctggacttcgtggccgttgcacccatgcacccatgcacccatgc
ctggacttcggcacaactccctggacttcgtggccgttgcacccatgcacccatgcacccatgc
50 aggaacctggccagctggacccatgcacccatgcacccatgcacccatgcacccatgcacccatgc
aagagccctggcagctgcgttccgggacaataacccatggccttcactggacccatgcacccatgc
ccgctggaaagccctggacttcgtggcaggaaaccatgcacccatgcacccatgcacccatgc
ctccagaagctggacccatgcacccatgcacccatgcacccatgcacccatgcacccatgc
atagagcttacccatgcacccatgcacccatgcacccatgcacccatgcacccatgc
55 aaaatccctagacgtgagcccaacccgtccactgcgcctgcggggcggcccttggacttcctgtgg
caggaggccgtgcccgggtgtccaggcgcgtcacatgtggcagtcggccagccatcc
acacaggacccatgcgccttcgttggatgagacccttccttggactgtttgg

- 15 -

SEQ ID NO:13 (Equine TLR9)

MGPCGHGALQPLSLLVQAAMLAVALAQGTLPPFLPCELQPHGLVNCNWLFLKSVPHFSAAAPRDNVTSLSLLSNRI
 5 HHLHSDFAQLSMLQKLNWKNCPPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLIL
 SRTNILQLDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNTTVPRSLPPSLEYL
 LLSYMHIVTЛАPEDLANLTALRVLDVGGNCRRCDHARNPCVECPHKFQQLHSDFSHLSRLEGVLKDSSLYQLN
 PRWFRGLGNLTVLDLSENFLYDCITKTAKAFQGLAQLRRLNLSFNYHKKVSFAHLLTAPSFGSLLSLQELDMHGIF
 10 FRSLSQKTLQPLARLPMQLQRLYLMQMFINQAOQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS
 RDLTPGPLDTPSSEDFMPSCKNLSFTLDSRNNLVTQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSQV
 15 LDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMSMRGVGHNLFSVVAQLPTLRLYSLAHTNGIHSRVSQQLCSTSL
 WALDFSGNSLSQMWAEGLYLRFFQGLRSLIRLDSLQNRLLHTLLPCTLGNLPKSLQLLRLRNNYLAFFNWSSLTL
 LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRSNSIIFVVPGFFALATRLRELNLSANALRTEEPSWFGFLAG
 SLEVLVDSANPLHCACGAAFDLQVQAAVPGLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFGSLLV
 VALGLAMPMLHHLCGWDLWYCFHGLAWLPRRGWQRGADALSYDAFVVFDAQSAVADWVYNELRVLEERRGR
 20 ALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDQVSGLLRASFLLAQQRLLLEDRKDVVVLVILSPDARR
 SRYVRLRQRLCRQSVLFWPHQPSGQRSFWAQLGMALTRDNRHFYNQNFCRGPTMAE

SEQ ID NO:14 (Equine TLR9)

MGPCGHGALQPLSLLVQAAMLAVALAQGTLPPFLPCELQPHGLVNCNWLFLKSVPHFSAAAPRDNVTSLSLLSNRI
 20 HHLHSDFAQLSMLQKLNWKNCPPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLIL
 SRTNILQLDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNTTVPRSLPPSLEYL
 LLSYMHIVTЛАPEDLANLTALRVLDVGGNCRRCDHARNPCVECPHKFQQLHSDFSHLSRLEGVLKDSSLYQLN
 PRWFRGLGNLTVLDLSENFLYDCITKTAKAFQGLAQLRRLNLSFNYHKKVSFAHLLTAPSFGSLLSLQELDMHGIF
 25 FRSLSQKTLQPLARLPMQLQRLYLMQMFINQAOQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS
 RDLTPGPLDTPSSEDFMPSCKNLSFTLDSRNNLVTQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSQV
 LDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMSMRGVGHNLFSVVAQLPTLRLYSLAHTNGIHSRVSQQLCSTSL
 WALDFSGNSLSQMWAEGLYLRFFQGLRSLIRLDSLQNRLLHTLLPCTLGNLPKSLQLLRLRNNYLAFFNWSSLTL
 LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRSNSIIFVVPGFFALATRLRELNLSANALRTEEPSWFGFLAG
 SLEVLVDSANPLHCACGAAFDLQVQAAVPGLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFG

30

SEQ ID NO:15 (Equine TLR9)

ctctgttctctgagctgtggccgcgtgaagggactgcgagcacaaggcatcctcctgcagctgtgtccccatgc
 tgccagctggaccctctggatcatctccactccctgtcatggcccttgcacatgtggccctgcagccccatgc
 35 ctccctggatgcaggccatgtggccgtggctctggcccaaggcaccctgcctccctgcctgcagctgc
 cagccccacggcgtgtgaactgcacactggctgtttctgaagtcgtgccccacttctcagcagcaccgg
 gacaatgtcaccagcccttcctgtctccaaaccgcacccacccatccacgcactccgactttgcacactgtcc
 aacctgcagaaactcaacccaaatggaaactgcggccagccggctcagcccatgcacttccctgcacatgc
 accatcgagccaaacactttctggctgtaccacccatggagactgtacacactgcacccatgcacact
 40 gtgcctgcctgcccagctccctcgatccctgtatccatgcacactgcacccatgcacccatgcacccatgc
 ctcacggccctgcacccctgcgttccatatacatggatggcaactgcactacaagaaccctgcgggggg
 ctggaggtggcccccaggcccttcctggcctggcaacccatccacccatgtcactcaactacaaccatgc
 acgggtggcccccagccctgcacccatgcacccatgcacccatgcacccatgcacccatgcacccatgc
 45 gaggacctggccaaatctgactgcctgcgtgtcgtatgtggggaaactgcggccctgtgaccatgcacgc
 aaccctgcgtggagtgcccacataaaattcccccagctgcactccgcacccatgcacccatgcacccatgc
 ggcctcggttgaaggataggctctctaccagactgcacccatgcacccatgcacccatgcacccatgc
 50 gacttccctggctgcgtacatagacccatgcacacaaccgcattccaggccctggccaggccatgc
 ctcgacccatgcgttgcacccatgcacccatgcacccatgcacccatgcacccatgcacccatgcacccatgc
 agactcaactgtcctcaattaccataagaagggtgtccctgcggccacccatgcacccatgcacccatgc
 ctgctccctgcacccatgcacccatgcacccatgcacccatgcacccatgcacccatgcacccatgc
 gcccgcctggccatgcacccatgcacccatgcacccatgcacccatgcacccatgcacccatgc
 gacttccctggctgcgtacatagacccatgcacacaaccgcattccaggccctggccaggccatgc
 ggggagggtggatggtgaaaagggtgtggctgcacatccaggccacccatccaggccactggacaccc
 tctgaggacttcatgccaagctgcacccatgcacccatgcacccatgcacccatgcacccatgc
 cagccagagatttgcccagctctcgccctccagtcgcctgcgcctgaggccacaacagcatctcg
 caggccgt

- 16 -

25

SEQ ID NO:16 (Equine TLR9)

- 17 -

cagggttcaggctgccgtgcctggctgcccagccgcgtcaagtgtggcagtcggccagctccagggccgcagc
atcttcgcacaagacacctgcgcctctgcctggacaagtcctctcctggactgttttgtt

SEQ ID NO:17 (Ovine TLR9)

5 MGPYCAPHPLSLLVQAAALAAALAQGTLPAFLPCELQPRGVNCNWFLKSVPFRSAGAPRANVTSLSLISNRH
HLHDSDFVHLSNLRVNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSSL
RTSILVLGPTHFTGLHALRFLYMDGNCYYKNPCQOAVEVAPGALLGLGNLTHLSLKYNNLTEVPRRLPPSLDTLL
LSYNHIITLAPEDLANLTALRVLVDVGGNCRRCDHARNPCRECPKNFPKLHPTDFSHLSRLEGLVLKDSSLYKLEK
DWFRGLGLRQVLIDLSENFLYDITKTTIFRNLTQRLRNLSFNYHKKVSFAHLQLAPSFGGLVSLEKLDMHGIFT
10 RSLNTTTLRPLTQLPKLQSLSLQLNFINQAEELSIFGAFPSLLFVLDLSDNRISGAARPVAALGEVDSGV
EVEVWRWPR GLAPGPLAAVSAKDFMPSCNLFNTLDLSRNLLVTIQQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRL
VLD LSYNKLDLYHGRSFTELPQLEALDLSYNSQFSMQGVGHNLSFVAQLPSLRLYLSLAHNGIHSRVSQKLSSASLRA
LDFSGNSLSQMWAEGLDLYLCFFKGLRNLVQLDLSKHNHLHTLLPRHLDNLPKSLRQLRLRDNNLAFFNWSSLTVLP
QLEALDLAGNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTGFFVLANRLKELNLSANALKTVDPFWFGRLTETL
15 NILDVSANPLHCACGAAVFDFLLEMQAAVPGLSRRVTGSPGQLQGRSISFAQDLRLCLDETLSDLCFGFSLLMVA
LGLAVPMLHHLCGWDLWYCFHLCLAHLPRRRQRGEDTLLYDAFVVFDAKAQSAVADWVYNELRVQLEERRGRAL
RLCLEERDWLPGKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQRLLLEDRKDVVVLVILRPAAYRSR
YVRLQRQLCRQSVLLWPHQPSQGSFWANLGMALTRDNRHFYNRNFCRGPTTAE

20 SEQ ID NO:18 (Ovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAQGTLPAFLPCELQPRGVNCNWFLKSVPFRSAGAPRANVTSLSLISNRH
HLHDSDFVHLSNLRVNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSSL
RTSILVLGPTHFTGLHALRFLYMDGNCYYKNPCQOAVEVAPGALLGLGNLTHLSLKYNNLTEVPRRLPPSLDTLL
LSYNHIITLAPEDLANLTALRVLVDVGGNCRRCDHARNPCRECPKNFPKLHPTDFSHLSRLEGLVLKDSSLYKLEK
DWFRGLGLRQVLIDLSENFLYDITKTTIFRNLTQRLRNLSFNYHKKVSFAHLQLAPSFGGLVSLEKLDMHGIFT
25 RSLNTTTLRPLTQLPKLQSLSLQLNFINQAEELSIFGAFPSLLFVLDLSDNRISGAARPVAALGEVDSGV
EVEVWRWPR GLAPGPLAAVSAKDFMPSCNLFNTLDLSRNLLVTIQQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRL
VLD LSYNKLDLYHGRSFTELPQLEALDLSYNSQFSMQGVGHNLSFVAQLPSLRLYLSLAHNGIHSRVSQKLSSASLRA
LDFSGNSLSQMWAEGLDLYLCFFKGLRNLVQLDLSKHNHLHTLLPRHLDNLPKSLRQLRLRDNNLAFFNWSSLTVLP
QLEALDLAGNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTGFFVLANRLKELNLSANALKTVDPFWFGRLTETL
30 NILDVSANPLHCACGAAVFDFLLEMQAAVPGLSRRVTGSPGQLQGRSISFAQDLRLCLDETLSDLCFG

SEQ ID NO:19 (Ovine TLR9)

gtcggcacggaaagttagcgccaaagcatcctccctgcagctgccgcacacttgcggccagacccctctggaga
35 agccgcattccctgccatggcccccactgtgccccgcacccctttctcctgtgcaggcggccgcgtgg
agcagccctggcccaggccacccgtccgccttcgtgcagctccagccccgggtaaggtaactgaa
ctggcttccctgaagtctgtccgcgtttcggccggagccccccggccaatgtcaccagccctccttaat
ctccaaccgcatccaccacttgcacgactctgacttcgtccacctgtccaaacctgcgggtcctcaaccta
40 gaactgccccggccggcctcagcccatgcacttccctgcccatgaccatcgagccaaacaccttcctgg
tgtgcccaccctggaggagctgaacctgagctacaatggcatcagccgtgcctgcctgcccagttctctgt
atccctgtcgctgagccgacccatcttgcgtgcaggccccacccacttcaccggcctgcacgcctgcgtt
tctgtacatggacggcaactgactataagaacccctgcccacggccgtggagggtggcccccaggccctc
tggcttggcaacccatcaccgcacctgtgcgtcaagtacaacaacctcaccggaggctggcaatctgactgc
45 cctggacaccctgtgtcctacaaccatcatcaccctggcaccggaggacccatgcggaggatgc
gcgtgtcgttgcgtggccggactgcgcggcgtgcgaccacgcggcccaacccctgcaggaggatgc
cttccccaagctgcaccctgacacccttgcggccacttgcggccctcgaaaggcctgggttgaagg
50 ctacaaaactagagaaagactgggtccgcggctggcaggcttcaactgtgcacccatgcgc
tgactacatcaccatcaccgcacccatcttgcgtgcaggatgcgcacactcaacccatgc
caagaaggatgccttcgcaccctgcacactggcacccttcgtggggccctgggtgc
gcacccatcttgcgtggccctcaccacaccgcgtccgcgtgacc
gatgcggcagacttgcacccatcaaccaggccgaggatgc
cctgtcgacccatcaccgcacccatcttgcgtgcaggatgc
ctggcggtggcccaaggggccctcgccaggcccgcgtgg
ctggccgcgtcagc
cagc
caaggacttcatgc
caagctgca

- 18 -

5 cctcaacttacacccgtggacctgtcacggaaacaacccgtgtacgatccaggcaggagatgttacccgcctccccc
cctccagtgcctgcgcctgagccacaacagcatctcgccaggcggttaatggctcgcatcgtgcgcctgaccgg
cctgcgagtgcctgcacccgtccataacaagctggacccgttaccatggcgctcgatcaggagctgcgcagct
ggaggcactggacccgtacatcacaacagccaggcccttcagcatgcaggcggtggccacaacccctcagttcg
ccagctgcgcctgcgcctacccgtacgcgcacaacccgtatccacagccgcgtgtcacagaagctcagcag
cgccctcgctgcgcgcctggacttcagccgcaactccctgagccagatgtggcccgaggagacccctatctcg
cttcttcaaggcttgagggacccgttccagctggacccgttccaaagaaaccacccctgcacaccctcctgcctcg
cctggataacccgtcccaagagccgtcgccgcagctgcgttccgggacaataacccgttccctcaactggagc
cctgactgttctgccccagctggaaagccctggatctggcgaaaaccagctgaaggccctgagcaacccgc
gccacccgtggacccggctccagaagctggacgtgagccgcacacccgtatccgcggccctgtgaccctggcttctgt
ccttgcacccggctgaaagagcttaacccgtccgcacccgttccctgtgatccctctggcttccgg
cttaacccggctgaaatccatccatccgcacccgttccctgtgatccctctggcttccgg
cttccctgtggagatgcaggccgcgttccctggctgtccaggcgctcactgtgcctgcggggcccttgg
ggccgcgcacatccatccgcacccggacttgcgccttgcctggatgagaccctcccttggactgttgg
gctgcataatggggcgctgggcctggcgccatgtgcaccaccctgtggctgggaccctgtggactgtt
ccacccgtgtctggccatccatccgcacccggacggccggccgcagccggccgaggacaccctgttccatgc
ggcttcgacaaggcgccagactgtcactggccactgggttacaacccgttccgcgtgcagctggaggagcc
ccggccgcggccgtccgccttgcctggaggagccgcagactggctccctggcaagacccgttccgc
ggctcggttccatccgcacccgttccatccgcgcgttccatccgcgc
cagttccctgtggccacccggccgcgcgttccatccgcgc
ccgcctaccggccggccgttccatccgcacccgttccatccgcgc
cagtggccagggttagcttctggccaaacccgttccatccgcgc
cttctgcggggcccaacccgttccatccgcgcacttctataaccgg
aa

25 SEQ ID NO:20 (Ovine TLR9)

- 19 -

caggcggccgtgcctgggctgtccaggcgctcacgtgtggcagtccggccagctccaggccgcacatcttc
gcacaggacctgcgcctctgcctggatgagacccttccttggactgcttggc

Complete nucleotide and amino acid sequences for canine and feline TLR9 are
5 publicly available. For example, an amino acid sequence for canine TLR9 is available as
GenBank accession number BAC65192 and its corresponding nucleotide sequence is
available as GenBank accession number AB104899. An amino acid sequence for feline
TLR9 is available as GenBank accession number AAN15751 and its corresponding
nucleotide sequence is available as GenBank accession number AY137581.

10 Complete nucleotide and amino acid sequences for canine and feline TLR9 were also
determined independently from those available from public databases.

An amino acid sequence of canine TLR9 is provided as SEQ ID NO:21. Based on
comparison with known amino acid sequences of human and murine TLR9, it appears that
SEQ ID NO:21 includes sequence for at least a majority of the extracellular domain, all of the
15 transmembrane domain, and at least a portion of the intracellular domain of canine TLR9
(See Figure 1). Amino acids numbered 1-822 of SEQ ID NO:21 are presumptively
extracellular domain and correspond to SEQ ID NO:22. SEQ ID NO:23 is a nucleotide
sequence of canine TLR9 cDNA having an open reading frame corresponding to nucleotides
91-3186. SEQ ID NO:24 is a nucleotide sequence of canine cDNA encoding amino acids 1-
20 822 of SEQ ID NO:21.

An amino acid sequence of feline TLR9 is provided as SEQ ID NO:25. Based on
comparison with known amino acid sequences of human and murine TLR9, it appears that
SEQ ID NO:25 includes sequence for at least a majority of the extracellular domain, all of the
transmembrane domain, and at least a portion of the intracellular domain of feline TLR9 (See
25 Figure 1). Amino acids numbered 1-820 of SEQ ID NO:25 are presumptively extracellular
domain and correspond to SEQ ID NO:26. SEQ ID NO:27 is a nucleotide sequence of feline
TLR9 cDNA having an open reading frame corresponding to nucleotides 87-3179. SEQ ID
NO:28 is a nucleotide sequence of feline cDNA encoding amino acids 1-820 of SEQ ID
NO:25.

30

SEQ ID NO:21 (Canine TLR9)

MGPCRGALHPLSLLVQAAALALALAQGTLPAFLPCELQPHGLVNCNWLFLKSVPRFSAAAPRGNVTSLSLYSNRI
HHLHDYDFVHFVHLRRLNLKWNCPPASLSPMHFPCHMTIEPNTFLAVPTLEDLNLSYNSITTVPALPSSLVSLSL
SRTNILVLDPATLAGLYALRFLFLDGNCYYKNPCQQALQVAPGALLGLGNLTHLSLKYNNLTVVPRGLPPSLEYL

- 20 -

LLSYNHIIITLAPEDLANLTALRVLVDGGNCRRCDHARNPCRECPKGFPQLHPNTFGHLSHLEGLVLRDSSLYSLD
 PRWFHGLGNLMVLDLSENFLYDCITKTAKAFYGLARLRLNLNFNYHKKVSAFHHLASSFGSLLSIQELDIHGIF
 5 FRSLSKTTLQSLAHLPMQLNLQNLNFIQSQAQLSIFGAFTPGLRYVDSLSDNRISGAAEPAATGEVEADCGERVWP
 QSRDLALGPLGTPGSEAFMPCRTLNFTLDLSRNLLTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL
 RVLDLSHNKLDLYHGRSFTELPRLEALDLSYNSQFMSMRGVGNLNSFVAQLPALRYLSLAHNGIHSRVSQQLRSA
 10 SLRALDFSGNTLSQMWAEGDLYLRFQGLRSLVQLDLSQNRLHTLLPRNLDNLPKSLRLLRLRDNYLAFFNWSSL
 ALLPKLEALDLAGNQLKALSNGSLPNTGQLQRLDLSGNSIGFVVPSFFALAVRLRELNLSANALKTVEPSWFGSL
 AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPGPLPSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWVCFSLSL
 LAVALSLAVPMILHQLCGWDLWYCFHLCIWLPRRGRRGVDALAYDAFVVFDKAQSSVADWVYNELRVQLEERRG
 15 RRALRLCLEERDWVPGKTLFENLWASVYSSRKTFLVARTDRVSGLLRASFLAQQLLEDRKDVVVLVILCPDA
 HRSRYVRLRQRLCRQSVLLWPHQPSGRSFWAQLGTALTRDNRHFYNQFCRGPTTA

SEQ ID NO:22 (Canine TLR9)

MGPCRGALHPLSLLVQAAALALALAAGQTLPAFLPCELQPHGLVNCNWFLKSVPRFSAAAPRGNVTSLSLYSNRI
 15 HHLHDYDFVHFVHLRRRNWKNCPPASLSPMHFPCHMTIEPNTFLAVPTLEDLNLSYNSITTVPALPSSLVSLSL
 SRTNIVLVDPATLAGLYALRFLFLDGNCCYKNPCQQALQVAPGALLGLGNLTHLSLKYNLLTVVPRGLPPSLEYL
 LLSYNHIIITLAPEDLANLTALRVLVDGGNCRRCDHARNPCRECPKGFPQLHPNTFGHLSHLEGLVLRDSSLYSLD
 PRWFHGLGNLMVLDLSENFLYDCITKTAKAFYGLARLRLNLNFNYHKKVSAFHHLASSFGSLLSIQELDIHGIF
 20 FRSLSKTTLQSLAHLPMQLNLQNLNFIQSQAQLSIFGAFTPGLRYVDSLSDNRISGAAEPAATGEVEADCGERVWP
 QSRDLALGPLGTPGSEAFMPCRTLNFTLDLSRNLLTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL
 RVLDLSHNKLDLYHGRSFTELPRLEALDLSYNSQFMSMRGVGNLNSFVAQLPALRYLSLAHNGIHSRVSQQLRSA
 SLRALDFSGNTLSQMWAEGDLYLRFQGLRSLVQLDLSQNRLHTLLPRNLDNLPKSLRLLRLRDNYLAFFNWSSL
 ALLPKLEALDLAGNQLKALSNGSLPNTGQLQRLDLSGNSIGFVVPSFFALAVRLRELNLSANALKTVEPSWFGSL
 25 AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPGPLPSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWVCFS

SEQ ID NO:23 (Canine TLR9)

aggaaggggctgtgagctccaaggcatccttcctgcagctgtcccagccagccagaccctctggagaag
 ccccccgtccctgtcatggggccctgcgcgtggccgcgtgcacccctgtctctcctgtgcaggctgcgcgtca
 30 gcccgtggccctggcccaggccaccctgcctgcgtccctgcgcgtgcacccctgtgcaggccatggcctggtaactgc
 aactggctttctcaagtccgtgcccgcgttcgcgcgtgcacccgcgttaacgtcaccaggcccttccttg
 tactccaaccgcatccaccacccatgcactatgactttgtccacttcgcgcgtctcaatctcaag
 tggaactgcccggccgcgcgtccatgcactttccctgtcacatgaccattgagcccaacacccctctg
 gctgtgcccacccttagaggacctgaatctgagctataacagcatcaccgcactgtgcccgcctgcccagttcgctt
 35 gtgtccctgtccctgagccgcaccaacatcctggctggaccctgcccgcaggccctgcagggtggcccaatgcctgcgc
 ttcctgttccctggatggcaactgctactacaagaaccctgcacccgcgtccatgcaggccctgcagggtggcccaatgcctgcgc
 ctggccctggcaacccatcacacacccatgcactcaactacaacaaccctcaccgtgggtgcggccggccctgcccccc
 agcctggagtagccctgtctgtcctacaaccatcatcaccctggccacccatgcaggccctgcagggtggcccaatctgactgcc
 40 ctgcgttcctcgatgtgggtggaaactgtgcgcgcgtgtgaccatgcccgttaaccctgcagggtggcccaatgcctgcgc
 ggctccccccagctgcaccccaacacccatggccacccatgcaggccatgcaggccctgggtttgaggagacagctct
 ctctacagccctggacccagggtggatccatggcctggcaacccatgggtgtggaccctgaggtaacttcctg
 tatgactgcatcacaaaaaccctacgcgtggccctggccggctgcgcgcactcaacccatgtccttcattat
 cataagaaggtgtcctttggccacccatgcacccatgcgtccctcggggactctgtccctgcaggagactggac
 atacatggcatcttcctcgatgcactcaagaccacgcgtccatgcgtccctggcccaatgcctgcaggccatgtcc
 45 ctgcatctgcaggtaacttgcacccatgcaggccatgcaggccatgcacccatgcgtccctggactgcgttgcgt
 gactgtcagacaaccgcacccatgcaggccatgcaggccatgcaggccatgcaggccatgcgtccctggactgtgg
 gagagagtctggccacaggccctggacccatgcgtccctggccactggccaccccccgcgtcaggccctcatgcgc
 agctgcaggaccctcaacttcacccatgcgtccctggacccatgcgtccctggccactggccatgcaggccatgttt
 cggctggccgcgcctccactgcgtccctggccactggccacccatgcgtccctggactgcgttgcgt
 50 cctctgagcaacccatgcgggtgtggaccctgcgtccctggacccatgcaggccatgcgtccctggactgcgttgcgt
 ctggccgcggccctggaggccctggacccatgcaggccatgcaggccatgcgtccctggactgcgttgcgt
 agctttgtggacccatgcgtccctggacccatgcaggccatgcgtccctggacccatgcaggccatgcgttgcgt
 cagctccgcaggccctgcgtccctggacccatgcgtccctggacccatgcaggccatgcgttgcgt
 ctctatctccgttcttccaaaggccctgagaaggccctgggttgcgtccctggacccatgcgtccctggactgcgttgcgt
 ctggccacccatgcggccatgcgtccctggacccatgcaggccatgcgtccctggactgcgttgcgt
 55 aactggaggccctggccctccatggacccatgcgtccctggacccatgcaggccatgcgttgcgt
 aactggaggccctggccctccatggacccatgcgtccctggacccatgcaggccatgcgttgcgt

- 21 -

aatggcagctgcccacggccacccagctccagggctggacactcagggcaacagcatcggttcgtggccccc
5 agctttttggccctggccgtgaggctcgagactcaacctcagggccaaacgcctcaagacggtgagccctcc
tggtttgggtccctggccgtgcccctgaaagtcttagacgtgaccggcaaccccttgcattgcgttgcggcga
accttcgtggacttctgtctggaggtgcaggctggccctgcttagccgtgtcaagtgcggcagcccg
ggccagctccaggggccgacatcttcgcacaggacactgcgcctctgctggacgaagcgctctccctgggtctgt
ttcagccctctcgctgtggctgtggccctgagcctggctgtgcaccagctctgtggctggacact
10 tggtaactgttccacctgtgcctggccctggctggccggggggccggccgggggtgtggatgcctggccat
gacgccttcgtggtcttcgacaaggcgacagactcggtggccgactgggtgtacaatgagctgcgggtacagcta
gaggagcggcgtggcgccggcgctacgcctgtgtctggaggaacgtgactgggtacccggaaaacccttc
15 gagaacactctggccctcagttacagcagccgcaagacgcgtttgtgtggccgcacggacagagtcagccgc
ctcctgcgtgccagcttcgtgtggcccaacagcgccctgtggaggaccgcacggacgtcggtgtggatgc
ctgtgcggccgcacccacgcgtcccgctatgtgcggctgcggccagcgccctgtgcggccagactgtccctctgg
ccccaccagccagtgccagcgcagctctggccagctggccacggccctgaccaggacaaccgcacttc
tacaaccagaacttcgtgcggggcccccacgcacagcctgtatggcagacagccagcacccgcacccatcc
20 ctgcctgtctgtggatgcggccacctgtggctctacaccgcgtctgtctccctacaccgcggccctggca
taaagcgaccgctcaataatgctgtggtagac

SEQ ID NO:24 (Canine TLR9)

SEO ID NO:25 (Feline TLR9)

55 MGPCHGALHPLSLLVQAAALAVALAQGTLPAFLPCELQRHGLVNCDWLFLKSVPHFSAAPRGNTSLSLYSNRI
HHLHDSDFVHLSSLRRLNLKWNCPPASLSPMHFPCHMTIEPHTFLAVPTLEELNLSYNSITTVPALPSSLVSLSL

- 22 -

SRTNIVLDPANLAGLHSRFLFLDGNCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL
 LLSYNHIITLAPEDLANLTALRVLVDVGGNCRRCDHARNPCMCECPKGFPHLHPDTFSHLNHLEGVLVKDSSLVYLN
 PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNYHKKVFAHLHAPSFGSLLSLQQLDMHGIF
 FRSLSETTLRSIVLHLPMLQSLHMQMFINQAOQLSIFGAFFPGLRYVDSLSDNRISGAMELAAATGEVDGGERVRLPS
 5 GDLALGPPGTPSSEGFMPCGCKTLNFTLDSLRSNNLVTIQPEMFARLSRLQCLLSSRNSISQAVNGSQFMPLTSILQV
 LDLSHNLKLDLYHGRSFTELPRLEALDLISYNSQPFMVGQVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASL
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNRLHTLLPRTLDNLPKSLRLLRLRDNYLAFFNWSSLV
 10 LPRLEALDLAGNQLKALSNGSLPNTGQLQRLDLSNSISFVASSFFALATRLRELNLSANALKTVEPSWFGSILAG
 TLKVLDVTGNPLHACGAAVFDFLLEVQAAVPGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCFGSLLT
 VALGLAVPMLHHLCGDLWYCFHLCALWLPRRGRRGADALPYDAFVFDAKAQSAVADWVYNELRVRLEERRGR
 ALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVIAHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILRPDAHR
 SRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNQHFYNQNFCRGPTTAE

SEQ ID NO:26 (Feline TLR9)

15 MGPCHGALHPLSLLVQAAALAVALAQGTLPAFLPCELQRHGLVNCDWLFLKSVPHSAAAPRGNVTSLSLYSNRI
 HHLHDSDFVHLSSLRRLNWKNCPPASLSPMHFPCHMTIEPHTFLAVPTLEELNLSYNSITTPALPSSLVSLSL
 SRTNIVLDPANLAGLHSRFLFLDGNCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL
 LLSYNHIITLAPEDLANLTALRVLVDVGGNCRRCDHARNPCMCECPKGFPHLHPDTFSHLNHLEGVLVKDSSLVYLN
 PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNYHKKVFAHLHAPSFGSLLSLQQLDMHGIF
 20 FRSLSETTLRSIVLHLPMLQSLHMQMFINQAOQLSIFGAFFPGLRYVDSLSDNRISGAMELAAATGEVDGGERVRLPS
 GDLALGPPGTPSSEGFMPCGCKTLNFTLDSLRSNNLVTIQPEMFARLSRLQCLLSSRNSISQAVNGSQFMPLTSILQV
 LDLSHNLKLDLYHGRSFTELPRLEALDLISYNSQPFMVGQVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASL
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNRLHTLLPRTLDNLPKSLRLLRLRDNYLAFFNWSSLV
 25 LPRLEALDLAGNQLKALSNGSLPNTGQLQRLDLSNSISFVASSFFALATRLRELNLSANALKTVEPSWFGSILAG
 TLKVLDVTGNPLHACGAAVFDFLLEVQAAVPGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCFG

SEQ ID NO:27 (Feline TLR9)

30 aggtctgcgagctccaggattttcttgccatcgctgccagtcgtccatccagaccctctggagaagcccc
 cactccctgtcatggggccctgccatggcccccgtctccatgggtcaggctgccgcgtggcc
 tggccctggcccaagggcacccctgcctgccttctgcctgtgagctccagcgcacggcgtgtgaattgcact
 ggcttccctcaagtccgtccccacttctcgccggcagcgcggccgtggtaacgtcaccgccttccctgtact
 ccaaccgcataccaccacccacgtccgactttgtccaccctgtccagctgcggcgtctcaacctaaatgga
 actgcccacccggccagccctcagccccatgcacttccctgtcacatgaccaattgagcccccacacccctctggcc
 tgccaccctggaggagctgaacctgagctacaacacatcacgacagtcaccgcgttccctgtgt
 35 ccgtccttgagccgtaccaacatccgtgtggaccctgcaacctcgccaggctgactccctgcgcgtt
 tggccctggatggcaactgtactacaagaacccctggccgcaggccctgcagggtggggggggccctcttg
 gcctggcaacccctacgcacccgtcactcaagtacaacaacccactcactgcgggtgccccggcctggggggcc
 tggagtacctgtattgtcctacaaccacatcataccctggccacctgaggacctggcaacctgaccgcctgc
 gtgtgcgtatgtgggtggactgcccgtcgctgtgaccacggccgcaacccctgtatggagtgcggccaagggt
 40 tccgcacccgtcaccctgacacccatggccacccgtacggccatccgtggatggccatccgttgcggcc
 acaacccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccat
 actgcacccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccat
 agaagggtgccttggccacccatggccatggccatggccatggccatggccatggccatggccatggccatggccat
 atggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccat
 45 acctgcagatgaacttcatcaatcggccatggccatggccatggccatggccatggccatggccatggccatggccat
 tggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccat
 ggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccat
 ccctcaacttcacccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccat
 gcctccaggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccat
 50 gcctccaggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccat
 gcctccaggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccat
 tggaggccctggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccat
 cacagctgcggccctgcgtatctcgcgtatctcgcgtatctcgcgtatctcgcgtatctcgcgtatctcgc
 ggcgtcgctgcggccctggacttcagccgtatctcgcgtatctcgcgtatctcgcgtatctcgcgtatctcgc
 acttctccgaggccctggacttcagccgtatctcgcgtatctcgcgtatctcgcgtatctcgcgtatctcgc
 55 ccctggacaacccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccatggccat

- 23 -

5 gcctggtcctcccccaggctggaagccctggacccctggcgaaaaccagctgaaggccctgagcaacggcagct
 tgcctaattggaaaccaggctccagaggctggacccctcagcagcaacagtatcagttcgccctccagtttttg
 ctctggccaccaggctgcgagagctcaacccctcagtgccaaacggccctcaagacggtgagccctctgggttcggtt
 ctctagggcaccctgaaagtccatgtactggcaacccctgcactgcccctgtggcccttcggactgg
 10 actcttgcggaggctgcaggctgcaggcccggctgcaggccacgttaaagtgtggcagttccaggtcagctcc
 agggccgcagcatcttgcggatctgcgcctctgcctggatgaggccctcttcggactgtttggccctct
 cgctgctgaccgtggccctggccgtgcccattgtgcaccacccctgtggctggacccctctggactgtct
 tccacctgtgcctggccctggctgccccgg
 15 tggcttcgacaaggcacagagcgcggggccactgggtgtacaacagactgcgggtacggctagaggagcgc
 gtggacgccgaggcgctccggctgtgcctggaggaaacgtactggctaccggtaaaacgcctttgagaacctgt
 gggccctcagtttacagcagggcagatgtgtttgtgtggccacacagacagggtcagcggccttgcgc
 ccagcttctgtgtggccctggccatgcggccctgtggaggacccgcaggacgttgtgtgtatcctgcgc
 acgcccaccgcctccgcataatgtgcggctgcgcctctgcgcaggagcgtccctctggccaccagc
 ccagtgccagcgcagttctggccctggccacggccctgaccaggacaaccagacttctataaccaga
 20 acttctgg
 ggtatgcgcgg

SEQ ID NO:28 (Feline TLR9)

20 atggggccctgcacatggcgccctgcacccctgtctctctggcaggctgcccgcgtggccgtggccctggcc
 cagggcaccctgcctgccttctgccttgcggctgtgagctccagcgcacggcctgtgtgaattgcgactggctgttcctc
 aagtccgtgccccacttctcggccgcagcgcggccctgtgttaacgtcaccaggcttccctgtactccaaccgcac
 caccacccctccacactccgactttgtccacctgtccagcgcctgcggcgctcaacccatggaaactgcccaccc
 gccagcctcagccccatgcacttccctgtcacatgaccattgagccccacaccccttgcgcgtgcgc
 25 gaggagctgaacctgagctacaacagcatcacgcacgcattccgcgcgttgcgcgttgcgcgttgcgc
 agccgttaccaacatcctgggtgtggacccctgccaacccctgcgcaggcgactccctgcgcgttgcgc
 ggcaactgtactacaagaacccctgcgcgcaggccctgcagggtggcccccggcgcccttgcgc
 cttacgcacctgtcactcaagtacaacacccatcactgcgggtgcgcgcgcgcgcgcgcgc
 30 ctattgtcctacaaccacatcatcaccctggcacctgaggaccctggccaaactgaccgcctgcgc
 gtgggtgggaactgcgcgtgtgaccacgcgcgcacccctgtatggagtgcgc
 caccctgacaccctcagccacactgaaccacccctgcgcaggccctgggttgcaggac
 cccagatggttccatgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc
 aaaaccacagccctccaggccctggccagctgcgcgcgcgcgcgcgcgc
 tttggccacctgcacatcggccgcgcgcgcgcgcgcgcgcgcgc
 35 ttccgc
 aacttcataatcaggccagactcagcatctcggccgcgcgcgcgcgc
 cgcataatggggccatggggactggccgcgcgcgcgcgcgcgc
 gggggacccatgttgcgcgcgcgcgcgcgcgcgcgcgc
 40 acctttggacccatgttgcgcgcgcgcgcgcgcgcgcgc
 ctggacccatgttgcgcgcgcgcgcgcgcgcgcgcgc
 gacccatgttgcgcgcgcgcgcgcgcgcgcgcgc
 45 ggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc
 ctcccccaagggcgcgcgcgcgcgcgcgcgcgc
 ctcccccaaggcgcgcgcgcgcgcgcgcgcgc
 50 gaggtgcaggctgcaggctgcaggccctgcgcgcgcgc
 atcttgcgcaggatctgcgcgcgcgcgcgcgcgc

Complete nucleotide and amino acid sequences for murine and human TLR9 are publicly available. For example, an amino acid sequence of murine TLR9 is available as

- 24 -

GenBank accession no. AAK29625, provided as SEQ ID NO:29. Amino acids numbered 1-821 of SEQ ID NO:29 presumptively include the entire extracellular domain and correspond to SEQ ID NO:30. SEQ ID NO:31 corresponds to GenBank accession number AF348140, which is a nucleotide sequence of murine TLR9 cDNA. SEQ ID NO:32 is a nucleotide sequence of murine cDNA encoding amino acids 1-821 of SEQ ID NO:29.

An amino acid sequence of human TLR9 is available as GenBank accession no. AAF78037, provided as SEQ ID NO:33. Amino acids numbered 1-820 of SEQ ID NO:33 presumptively include the entire extracellular domain and correspond to SEQ ID NO:34. SEQ ID NO:35 corresponds to GenBank accession number AF245704, which is a nucleotide sequence of human TLR9 cDNA. SEQ ID NO:36 is a nucleotide sequence of human cDNA encoding amino acids 1-820 of SEQ ID NO:33.

SEQ ID NO:29 (Murine TLR9)

15 MVLRRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAACSNITRLSLISNRI
HHLHNSDFVHLSNLRQLNLKWCNCPTGLSPHLFSCHMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSL
SHTNILVLDANSLAGLYSLRVLFMDGNCCYKNPCTGAVKVTGALLGLSNLTHLSLKYNNLTKVPRQLPPSLEYL
LVSYNLIVKLGPEDLANLTSRVLVDVGGNCRRCDHAPNPCIIECGQKSLHLHPETFHHLSHLEGLVLDKSSLHTLN
SSWFQGLVNLSVLDLSENFLYESINHTNAFQNLTRLRKLNLSFNYRKVSFARLHASSFKNLVSLQELNMNGIF
FRSLNKYTLRWLADLPKLHTLHQMNFINQALQLSIFGTFRALRFVDSLDRNISGPSTLSEATPEEADDAEQEELL
20 SADPHPAPLSTPASKNFMDRCKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ
VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFMSMKIGHNFSVAHLSMLHSLSLAHNDIHTRVSSHLNSNS
VRFLDFSGNGMGRMWDEGGYLHFFQGLSGLLKLDLSQNNLHLIRPQNLNDNLPKSLKLLSLRDNYLSFFNWTSL
FLPNLEVLDLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVPAFFALAVELKEVNLSHNLKTVDRSWFGPIV
25 MNLTVDVRSNPLHCACGAAFDVLLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFG
AVAVGMVVPILHHLCGWDVWYCFHLCLAWLPLLARSRRSAQALPYDAFVVFDKAQSADWVYNELRVLEERRG
RRALRLCLEDRDWLPGQTLFENLWASIVYGSRKTLFVLAHTDRVSGLLRTSFLLAQQRLLLEDRKDVVVLVILRPDA
HRSRYVRLQRQLCRQSVLFWPQQPNGQGGFWAQLSTALTRDNRHFYNQNFCRGPTAE

SEQ ID NO:30 (Murine TLR9)

30 MVLRRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAACSNITRLSLISNRI
HHLHNSDFVHLSNLRQLNLKWCNCPTGLSPHLFSCHMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSL
SHTNILVLDANSLAGLYSLRVLFMDGNCCYKNPCTGAVKVTGALLGLSNLTHLSLKYNNLTKVPRQLPPSLEYL
LVSYNLIVKLGPEDLANLTSRVLVDVGGNCRRCDHAPNPCIIECGQKSLHLHPETFHHLSHLEGLVLDKSSLHTLN
SSWFQGLVNLSVLDLSENFLYESINHTNAFQNLTRLRKLNLSFNYRKVSFARLHASSFKNLVSLQELNMNGIF
FRSLNKYTLRWLADLPKLHTLHQMNFINQALQLSIFGTFRALRFVDSLDRNISGPSTLSEATPEEADDAEQEELL
35 SADPHPAPLSTPASKNFMDRCKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ
VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFMSMKIGHNFSVAHLSMLHSLSLAHNDIHTRVSSHLNSNS
VRFLDFSGNGMGRMWDEGGYLHFFQGLSGLLKLDLSQNNLHLIRPQNLNDNLPKSLKLLSLRDNYLSFFNWTSL
FLPNLEVLDLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVPAFFALAVELKEVNLSHNLKTVDRSWFGPIV
40 MNLTVDVRSNPLHCACGAAFDVLLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFG

SEQ ID NO:31 (Murine TLR9)

tgtcagagggagccctgggagaatcctccatctccaaacatggttccgtcgaaggactctgcaccccttgc
ctcctggtagaggctgcagtgcggctgagactctggccctgggtaccctgcctgcctaccctgtgagctg

- 25 -

aaggcctatggcctggactgcaattggctgtccctgaaggtctgtaccccgttctcgccggcagcatccctgc
tccaacatcacccgccttccttgcatactccaaaccgtatccaccacccgtcacaactccgacttcgtccacccgtcc
aacctgcggcagctgaacctcaagtggaactgtccaccactggccttagccccctgcacttcttgcacatgc
accattgagccccagaaccttcctggctatgcgtacactggaggagctgaacctgagctataatggtatcaccact
5 gtcccccgactgcccagctccctggtaatctgagccctgagccacacaatccctggcttagatgctaaccaggc
ctcgccggcctatacaggcctgcgcgtcttcctatggacgggaactgtactacaagaaccctgcacaggagcg
gtgaagggtgaccccaggcccttcctggcctgagcaatctcaccatctgtcttgcagttataacaaccctcaca
aagggtgccccgccaactgccccccagcctggagttaccccttgcgttgcataacccttgcataagctggggct
gaagacctggccaatctgaccccttcgagttacttgcattggggattgcgtcgctgcaccatgcccc
10 aatccctgtatagaatgtggccaaaagtccctccacctgcaccctgagacccttccatcacctgagccatctggaa
ggcctgggtgtgaaggacagctctccatacactgaacttccctgttccaaaggctggtaaccctctcggt
ctggacctaagcgagaacttcttgcataaccacccaatgccttgcagaaccctaccctgc
aagctcaaccctgtccctcaattaccgcaagaaggatccttgcggccctccacctggcaaggcttgcataagaac
ctgggtcactgcaggagctgaacatgaacccgcatttcctccgcgtcaacaaggatcacgcctcagatggctg
15 gccgatctgcccacttccacactctgcattctcaaatgaacttcatcaaccaggcactgcacatcttgc
acttcccgagcccttcgcttgcgttgcagacaatgcattcaggcccttcaacgcgtcagaaggccacc
ccctgaagaggcagatgtgcagagcaggaggactgttgcggatccctcaccaggactccactgagccacc
gcttctaaagaacttcatggacagggttaagaacttcaagttcaccatggacccgtctcggaacaaccctggact
atcaaggccagagatgtttgtcaatcttcacccctccagttgccttagccacaactccattgcacaggct
20 gtcaatggcttcagttccctggcgtactaatctgcagggtgcgttgccttgcataactggacttgtac
cactggaaatcggtcagttgcagttgcaggccctggacccgttgcagttacaacaggccaggcccttgc
aagggtataggccacaatttcagtttgcgttgcctcatgcatacaccgccttgcgttgcacacaatgac
attcataccctgtgtcctcatactcaacacagactcagttgcgttgccttagccacaactccattgcacaggct
25 cgcattgtggatggggggcccttgcataatccctccatgcataactggacttgcgttgccttgcataactggacttgt
caaaaataaccctgcataatccctccggcccccagaacccttgcataactggacttgcgttgccttgc
gacaactaccctatccctttaactggaccaggctgtccctccctgcataactggacttgcgttgc
aaccaggctaaaggccctgaccaatggccaccctgcataatggccacccttgcataactggatgtc
atgcataactggacttgcgttgccttgcataactggacttgcgttgccttagccacaactccatt
ctcaagacgggttgcataactggacttgcgttgccttgcataactggacttgcgttgccttgc
30 ctgcactgtgcctgtggggcagccctcgttagacttactgttgcgttgcagaccaggacttgc
gggtgtgaagggtggtggcagccctggccagctgcaggccgttagcatcttcgcacaggacccgttgc
gaggtccctcttgcgttgccttgcataacttgcgttgcgttgccttgcataacttgc
catcttcgcgttgcgttgcataacttgcgttgccttgcataacttgcgttgc
35 cgcaggcccaagctccctatgcattgccttgcgttgcataaggc
tataacggactgcgggtgcggctggaggagcggcggcgtcccgagccctacgc
tggctgcctggccagacgccttcgcataacccttgcgttgccttgcataacttgc
gcccacacggaccgcgtcaggcccttgcgcaccaggacttgcgttgc
aaggacgtgggtgtggatccgcgtcccgatccaccgc
tgcgcctccaggcaggcccaacggcaggggggcttgcgttgc
ctgactaggacaaccgcacttgcataaccagaacttgcgttgc
gctggaaacagactgcattcatgcctggccaggactacagg
40 cagaatagctcagagaaca
gctggaaacagactgcattcatgcctggccaggacttgc
ctgcgttgc

SEQ ID NO:31 (Murine TLR9)

45 atggttctccgtcgaggactctgcaccccttgcctgtccctcctggatcaggctgcagtgcggctgagactctggcc
ctgggtaccctgcctgccttcacctgtgagctgaagccatggcctggactgcataattggctgttcctg
aagtctgtacccgttctctgcggcagcatcctgtccaaatcaccgccttcctgtatctccaaaccgtatc
caccacctgcacaactccgacttcgtccacctgtccaaacctgcggcagctgaacctcaagtggactgtccacc
actggccttagccccctgcacttcttgcacatgaccattgagccagaaccttctggctatgcgtacactg
50 gaggagctgaacctgagctataatggtatcaccactgtgccccactgcccagctccctggtaatctgaggctg
agccacaccaacatcctggttctagatgctaacagcctgcggcctatacagcctgcgttctcttcatggac
gggaactgtaactacaagaacccctgcacaggagcggtaaggtgaccccaaggcgcctctggcctgagacaat
ctcaccatctgtctctgaagtataacaacctcacaagggtccccgccaactgccccccagctggagtaacct
ctggtgtccataacctcattgtcaagctggggctgaagacctggccaatctgaccccttcagtagacttcat
55 gtgggtggattgcgtcgctgcgaccatgcccccaatccctgtatagaatgtggccaaaggccctccacctg
caccctgagacccatcacctgagccatctggaaggcctggctgaaggacagctctccatcacactgaac
tcttctgggtccaaaggctggtaacacctcgtgtctggacctaagcgagaacttctctatgaaagcatcaac
cacaccaatgccttcagaacctaaacctgcgtcgcaagctcaacctgtccattaccgcaagaaggatcc

- 26 -

5 tttggccgcctccacctggcaagttccctcaagaacactggtcactgcaggagctgaacatgaacggcatcttc
 ttccgcgtcaacaaggtaacacgcgtcagatggctggccgatctgcccactccacactctgcacatctcaaatg
 aactcatcaaccaggcacagctcagatcttgcacccctcgagccctcgctttgtggacttgcagacaat
 cgcatcagtgggcctcaacgcgtcagaagccacccctgaagaggcagatgtcagagcaggaggagcttt
 10 tctgcggatcctcaccctggactccactgagcacccctgttcaagaacttcatggacagggttaagaacttcaag
 ttcaccatggacactgtctcggacaacaacctggactatcaaggcagagatgtttgtcaatctctacgcctccag
 tgtcttagcctgagccacaactccattgcacaggctgtcaatggctcaggcttgcactaattctgcag
 gtgcggacactgtccataacaaactggacttgcacttgcaggaaatcgttcagtgcactaccacagttcaggcc
 ctggacctgagctacaacagccagcccttagcatgaagggtataggccacaatttcagtttgcggccatctg
 15 tccatgctacacagccttagcctggcacacaatgacattcataccgtgtgcctcacatctcaacagcaactca
 gtgagggttcttgacttcagcggcaacggatggccgcatgtggatgagggggcccttatctccatttctc
 caaggcctgagtgccctgtcaagctgacactgtctcaaaaataacctgcataatcctccggccccagaaccttgc
 aaccccccacagagcctgaagctgtcggacttgcaggcacaactacctatctttaactggaccagctgtcc
 20 ttcctgcccacactggaaactccttagcactggcaggcaaccactaaaggccctgaccaatggcaccctgcctaa
 ggcaccctccctccagaaactggatgtcagcagcaacagtatcgtctctgtggtcccagcccttgcctctggc
 gtcgagctgaaagaggtcaacctcagccacaacattctcaagacggatgcgtcttgcggatggccatttg
 atgaacactgacagtcttagcgtgagaagcaaccctctgacactgtgcctgtggcagccctgcgtagacttactg
 ttggaggtgcagaccaaggcctggctggctaattggatgtggcagcccccggcagctgcaggccgt
 25 agcatcttcgcacaggacccctggcgtgcctggatgaggtcctcttggactgcatttgc
 SEQ ID NO:33 (Human TLR9)

MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFMSMAAPRGNVTSLSLSSNRI
 HHLHDSDFAHLPPLRHLNLKWNCPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLISL
 25 SHTNIMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYL
 LLSYNRIVKLAPEDLANLTALRVLVDVGNCRRCDHAPNPMECPRFHFPQLHPDTFSHLRLEGLVLDSSLSWLN
 ASWFRGLGNLRLVLDLSENFLYKCITKTKAFQGLTQLRKLNLSPNYQKRVSPAHLSLAPSFGSLVALKELEDMHGIF
 FRSLDETTLRPLARLPMLQTLRLQMNFINQAOQLGIFRAFPGLRYVDSLSDNRIISGASELTATMGEADGGEKVWLQP
 GDLAPAPVDTPSSEDFRPNCASTLNFTLDSLRSRNNLVTQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV
 30 LDLSRNKLDLYHEHSFTELPRLEALDLISYNQPGMVGQVGHNFSPV AHLRLRHLSLAHNNIHSQVSQQLCSTSL
 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRRLDNYLAFFKWWSLHF
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLAS
 35 ALQILDVSANPLHCACGAAFMDFLLEQAVPGLPSRVKCGSPGQLQGLSIFAQDRLCLDEALSWDCFALSILIA
 VALGLGVPMMLHLCWDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDTQSAVADWVYNELRGQLEECRG
 RWALRLCLEERDWLPGKTLFENLWASVYGSRKTFLVLAHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILSPDG
 RRSRYVRLQRQLCQSVLLWPHQPSGQRSFWAQLGMALTRDNHHFYNRNFQCGPTAE

SEQ ID NO:34 (Human TLR9)

MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFMSMAAPRGNVTSLSLSSNRI
 HHLHDSDFAHLPPLRHLNLKWNCPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLISL
 40 SHTNIMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYL
 LLSYNRIVKLAPEDLANLTALRVLVDVGNCRRCDHAPNPMECPRFHFPQLHPDTFSHLRLEGLVLDSSLSWLN
 ASWFRGLGNLRLVLDLSENFLYKCITKTKAFQGLTQLRKLNLSPNYQKRVSPAHLSLAPSFGSLVALKELEDMHGIF
 FRSLDETTLRPLARLPMLQTLRLQMNFINQAOQLGIFRAFPGLRYVDSLSDNRIISGASELTATMGEADGGEKVWLQP
 GDLAPAPVDTPSSEDFRPNCASTLNFTLDSLRSRNNLVTQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV
 45 LDLSRNKLDLYHEHSFTELPRLEALDLISYNQPGMVGQVGHNFSPV AHLRLRHLSLAHNNIHSQVSQQLCSTSL
 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRRLDNYLAFFKWWSLHF
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLAS
 ALQILDVSANPLHCACGAAFMDFLLEQAVPGLPSRVKCGSPGQLQGLSIFAQDRLCLDEALSWDCF

50 SEQ ID NO:35 (Human TLR9)

aggctggataaaaatcttacttcttattctctgagccgcgtgctgcccctgtggaaagggacccgtgactgtga
 agcatccttccctgttagctgtccagtcgtccggccagaccctctggagaagccctgccccccagcatgggt
 ttctgcccgcagccctgcacccgtctctcttgcaggccatcatgtggccatgaccctggccctgggt

- 27 -

SEQ ID NO:36 (Human TLR9)

45 atgggtttctggcccgacggccctgcacccgctgtctcttggcggccatcatgtctggccatgaccctggcc
 ctgggtaccttgcctgccttccatccctgtgagctccagccccacggccctggtaactgcaactggctgttctg
 aagtctgtgccccacttccatggcagcaccggctggcaatgtcaccagccttctgtctccaaacccgcatc
 caccacccatgatttgcacttgcaccctggccagctggcatctcaacccatcaacttgcgaactggccggccg
 gttggcctcagccccatgcacttccctggccacatgaccatcgagccagcaccttggctgtgcccaccctg
 50 gaagagctaaacctgagctacaacaacatcatgactgtgctgcgcgtccaaatccctcatatccctgtccctc
 agccataccacatccatgtgactctgcgcagccctgcggccctgcatgcctgcgttccattcatggac
 ggcactgttattacaagaacccctgcagggcaggactggaggtggcccccgggtgccttgcctggccctggcaac
 ctcacccacccgtcactcaagtacaacaacccactgtggtgcggccacccctgcatggagtgcccttgcgttgc
 55 ctgttgcctacaaccgcacgtcaaactggccctggacactggccatctgaccgcctgcgtgtgcgtcat
 gtggccggaaattggccggctgcgaccacgcctccaaacccctgcatggagtgccctgcgtacttcccaac
 catcccgatacccttgcggccacccgtggccatgttgcggccatgttgcgttgcgtcat
 gccatgggttccctggccggaaacctccggactgtggacactggagtgacttgcgttgcgtcat

5 aaaacaaggccttccaggccctaacacagctgcgaagcttaacctgtccttcaattacccaaaagagggtgtcc
tttgcccacctgtctctggcccttccttcggagcctggctcgccctgaaggagctggacatgcacggcatcttc
ttccgctactcgatgagaccacgctccggccactggcccgcctgcccattgtctccagactctgcgtctgcagatg
aacttcatcaaccaggcccagctggcatcttcagggcttcctggctgcctacgtggacactgtcgacatgc
10 cgcatcagcgagcttcggagctgacagccaccatgggggaggcagatggagggagaaggtctggctgcagac
ggggaccttgcctccggcccccagtggacactcccagctctgaagacttcaggcccaactgcagcacccctcaacttc
acctggatctgtacggacaacactggtgaccgtgcagccggagatgtttgcctcgcacactgcagtg
15 ctgcgcctgagccacaactgcatctcgaggcagtcaatggctccagttcctgcctgcacccggctgcaggtg
ctagacctgtcccgcaataagctggaccttaccacgagcacttacacggacttgcgacttggaggccctg
gacctcagctacaacagccagcccttggcatgcagggctggccacaacttcagttcgtggctcacctgcgc
20 accctgcggccacctcagccctggccacaacacatccacagccaagtgtcccgacgcgtctgcagta
cgggccctggacttcagcgcaatgcactggccatatgtggccgagggagacctctatctgcacttctccaa
ggcctgagcggtttgatctggctggacttgcctccagaaccgcctgcacaccctcctggcccaaaaccctgcgc
ctcccaagagcctacaggtgctgcgtccgtgacaattactggctttaagtggtgagccctccacttc
ctgcccacacttggaaacttgcgtccgcacttgcagggaaaccggctgaaggccctgaccaatggc
accggctccggaggctggatgtcagtcacagcatcagttcgtggcccccggcttctttccaaggccaag
gagctgcgagagctcaaccttagcgccaaacgcctcaagacagtcggaccacttgcacttggcccttgg
25 gcctgcaaatactagatgtaaagcgccaaaccccttcgacttcgcctgtggggccctttag
gaggtgcaggctgcgtccgtctggccaggccgtgaagtgtggcagtcggccagctccaggcc
atcttgcacaggacctgcgccttcgcctggatgaggcccttcgcctggactgtttcgcc

In addition to the foregoing native rat, porcine, bovine, equine, and ovine TLR9 polypeptides and nucleic acid molecules encoding them, chimeric TLR9 polypeptides and nucleic acid molecules encoding them are provided by the invention. The chimeric polypeptides include at least one amino acid substitution based on a comparison of conserved and non-conserved amino acids among at least two of rat, murine, porcine, bovine, equine, ovine, canine, feline, and human TLR9. The information contained in a multiple sequence alignment of these various TLR9 polypeptide sequences, provided for example in Figure 1, can be used to identify and select individual amino acid positions and even individual amino acids to substitute in designing a chimeric TLR9. The substitution or substitutions can be effected using methods known to those of ordinary skill in molecular biology. Nucleic acids encoding the native or chimeric polypeptides of the invention can be inserted into an expression vector and used to express TLR9 polypeptide.

A conservative amino acid substitution shall refer to a substitution of a first amino acid for a second amino acid, wherein side chains of the first amino acid and the second amino acid share similar features in terms of hydrophobicity, size, aromaticity, or tendency to alter conformation. For example, conservative amino acid substitutions generally may be made between members within each of the following groups: hydrophobic (A, I, L, M, V), neutral (C, S, T), acidic (D, E), basic (H, K, N, Q, R), and aromatic (F, W, Y). A non-conservative amino acid substitution refers to any other amino acid substitution.

- 29 -

An expression vector for TLR9 will include at least a nucleotide sequence coding for a TLR9, or a fragment thereof coding for a functional TLR9 polypeptide, operably linked to a gene expression sequence which can direct the expression of the TLR9 nucleic acid within a eukaryotic or prokaryotic cell. A "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the nucleic acid to which it is operably linked.

With respect to TLR9 nucleic acid, the "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the TLR9 nucleic acid to which it is operably linked.

The gene expression sequence may, for example, be a mammalian or viral promoter, such as a constitutive or inducible promoter. Constitutive mammalian promoters include, but are not limited to, the promoters for the following genes: hypoxanthine phosphoribosyl transferase (HPRT), adenosine deaminase, pyruvate kinase, β -actin promoter, and other constitutive promoters. Exemplary viral promoters which function constitutively in eukaryotic cells include, for example, promoters from the simian virus (e.g., SV40), papillomavirus, adenovirus, human immunodeficiency virus (HIV), Rous sarcoma virus (RSV), cytomegalovirus (CMV), the long terminal repeats (LTR) of Moloney murine leukemia virus and other retroviruses, and the thymidine kinase (TK) promoter of herpes simplex virus. Other constitutive promoters are known to those of ordinary skill in the art.

The promoters useful as gene expression sequences of the invention also include inducible promoters. Inducible promoters are expressed in the presence of an inducing agent. For example, the metallothionein (MT) promoter is induced to promote transcription and translation in the presence of certain metal ions. Other inducible promoters are known to those of ordinary skill in the art.

In general, the gene expression sequence shall include, as necessary, 5' non-transcribing and 5' non-translating sequences involved with the initiation of transcription and translation, respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribing sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined nucleic acid coding sequence for a TLR9 polypeptide. The gene expression sequences optionally include enhancer sequences or upstream activator sequences as desired.

Generally a nucleic acid coding sequence and a gene expression sequence are said to be "operably linked" when they are covalently linked in such a way as to place the transcription and/or translation of the nucleic acid coding sequence under the influence or control of the gene expression sequence. Thus the TLR9 nucleic acid coding sequence and the gene expression sequence are said to be "operably linked" when they are covalently linked in such a way as to place the transcription and/or translation of the TLR9 nucleic acid coding sequence under the influence or control of the gene expression sequence. If it is desired that the TLR9 sequence be translated into a functional protein, two DNA sequences are said to be operably linked if induction of a promoter in the 5' gene expression sequence results in the transcription of the TLR9 sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the TLR9 sequence, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a gene expression sequence would be operably linked to a TLR9 nucleic acid sequence if the gene expression sequence were capable of effecting transcription of that TLR9 nucleic acid sequence such that the resulting transcript might be translated into the desired TLR9 protein or polypeptide.

A "TLR9 ligand" as used herein refers to a molecule that specifically binds a TLR9 polypeptide. In one embodiment the TLR9 ligand specifically binds a TLR9 polypeptide corresponding to at least a ligand-binding portion of the extracellular domain of TLR9. In most instances a TLR9 ligand will also induce TLR9 signaling when contacted with TLR9 under suitable conditions. TLR9 signaling refers to TLR/IL-1R signal transduction mediated through the TLR9, as described in further detail elsewhere herein. As mentioned above, CpG nucleic acids have been reported to be TLR9 ligands, but TLR9 ligands may include other entities as well, including, for example, small molecules. As also previously mentioned, there appears to be a species-specific preference for at least certain TLR9s and certain CpG motifs. As used herein, a species-preferred CpG DNA refers to a particular CpG DNA that is optimized for signal induction by a TLR9 of a particular species. A CpG DNA that is optimized for signal induction by a TLR9 of a particular species refers to a CpG DNA having a sequence that preferentially binds to and/or induces signaling by TLR9 of that species. For example, a human-preferred CpG DNA shall refer to a CpG DNA that optimally stimulates human TLR9 to signal through its TIR domain. Likewise, a murine-preferred CpG DNA

shall refer to a CpG DNA that optimally stimulates murine TLR9 to signal through its TIR domain. Examples of human-preferred and murine-preferred CpG DNA are ODN 2006 (SEQ ID NO:58) and 1668 (SEQ ID NO:60), respectively.

The binding and species specificity of TLR9s are believed to be influenced by key 5 amino acids present in the extracellular domain of TLR9. Key amino acids in a TLR9 as used herein refer to those amino acids which contribute significantly to ligand binding and ligand specificity of a particular TLR9 polypeptide.

A “CpG nucleic acid” or a “CpG immunostimulatory nucleic acid” as used herein is a nucleic acid containing at least one unmethylated CpG dinucleotide (cytosine-guanine 10 dinucleotide sequence, i.e., “CpG DNA” or DNA containing a 5' cytosine followed by 3' guanine and linked by a phosphate bond) which activates a component of the immune system. The entire CpG nucleic acid can be unmethylated or portions may be unmethylated but at least the C of the 5' CG 3' must be unmethylated.

In one embodiment a CpG nucleic acid is represented by at least the formula:

15 $5'-N_1X_1CGX_2N_2-3'$

wherein X_1 and X_2 are nucleotides, N is any nucleotide, and N_1 and N_2 are nucleic acid sequences composed of from about 0-25 N 's each. In some embodiments X_1 is adenine, guanine, or thymine and/or X_2 is cytosine, adenine, or thymine. In other embodiments X_1 is cytosine and/or X_2 is guanine.

20 Nucleic acids having modified backbones, such as phosphorothioate backbones, also fall within the class of immunostimulatory nucleic acids. U.S. Pat. Nos. 5,723,335 and 5,663,153 issued to Hutcherson, et al. and related PCT publication WO95/26204 describe immune stimulation using phosphorothioate oligonucleotide analogues. These patents describe the ability of the phosphorothioate backbone to stimulate an immune response in a 25 non-sequence specific manner.

An immunostimulatory nucleic acid molecule, including for example a CpG DNA, may be double-stranded or single-stranded. Generally, double-stranded molecules may be more stable *in vivo*, while single-stranded molecules may have increased activity. The terms “nucleic acid” and “oligonucleotide” refer to multiple nucleotides (i.e., molecules comprising 30 a sugar (e.g., ribose or deoxyribose) linked to a phosphate group and to an exchangeable organic base, which is either a substituted pyrimidine (e.g., cytosine (C), thymine (T) or uracil (U)) or a substituted purine (e.g., adenine (A) or guanine (G)) or a modified base. As

used herein, the terms "nucleic acid" and "oligonucleotide" refer to oligoribonucleotides as well as oligodeoxyribonucleotides. The terms shall also include polynucleosides (i.e., a polynucleotide minus the phosphate) and any other organic base-containing polymer. The terms "nucleic acid" and "oligonucleotide" also encompass nucleic acids or oligonucleotides with a covalently modified base and/or sugar. For example, they include nucleic acids having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 2' position and other than a phosphate group at the 5' position. Thus modified nucleic acids may include a 2'-O-alkylated ribose group. In addition, modified nucleic acids may include sugars such as arabinose instead of ribose. Thus the nucleic acids may be heterogeneous in backbone composition thereby containing any possible combination of polymer units linked together such as peptide-nucleic acids (which have amino acid backbone with nucleic acid bases). In some embodiments the nucleic acids are homogeneous in backbone composition.

The substituted purines and pyrimidines of the immunostimulatory nucleic acids include standard purines and pyrimidines such as cytosine as well as base analogs such as C-5 propyne substituted bases. Wagner RW et al. (1996) *Nat Biotechnol* 14:840-4. Purines and pyrimidines include but are not limited to adenine, cytosine, guanine, thymine, 5-methylcytosine, 2-aminopurine, 2-amino-6-chloropurine, 2,6-diaminopurine, hypoxanthine, and other naturally and non-naturally occurring nucleobases, substituted and unsubstituted aromatic moieties.

The immunostimulatory nucleic acid is a linked polymer of bases or nucleotides. As used herein with respect to linked units of a nucleic acid, "linked" or "linkage" means two entities are bound to one another by any physicochemical means. Any linkage known to those of ordinary skill in the art, covalent or non-covalent, is embraced. Such linkages are well known to those of ordinary skill in the art. Natural linkages, which are those ordinarily found in nature connecting the individual units of a nucleic acid, are most common. The individual units of a nucleic acid may be linked, however, by synthetic or modified linkages.

Whenever a nucleic acid is represented by a sequence of letters it will be understood that the nucleotides are in 5' to 3' (or equivalent) order from left to right and that "A" denotes adenine, "C" denotes cytosine, "G" denotes guanine, "T" denotes thymidine, and "U" denotes uracil unless otherwise noted.

- 33 -

5 Immunostimulatory nucleic acid molecules useful according to the invention can be obtained from natural nucleic acid sources (e.g., genomic nuclear or mitochondrial DNA or cDNA), or are synthetic (e.g., produced by oligonucleotide synthesis). Nucleic acids isolated from existing nucleic acid sources are referred to herein as native, natural, or isolated nucleic acids. The nucleic acids useful according to the invention may be isolated from any source, including eukaryotic sources, prokaryotic sources, nuclear DNA, mitochondrial DNA, etc. Thus, the term nucleic acid encompasses both synthetic and isolated nucleic acids.

10 The immunostimulatory nucleic acids can be produced on a large scale in plasmids, (see *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989) and separated into smaller pieces or administered whole. After being administered to a subject the plasmid can be degraded into oligonucleotides. One skilled in the art can purify viral, bacterial, eukaryotic, etc. nucleic acids using standard techniques, such as those employing restriction enzymes, exonucleases or endonucleases.

15 For use in the instant invention, the immunostimulatory nucleic acids can be synthesized *de novo* using any of a number of procedures well known in the art. For example, the β -cyanoethyl phosphoramidite method (Beaucage SL and Caruthers MH, *Tetrahedron Lett* 22:1859 (1981)); nucleoside H-phosphonate method (Garegg et al., *Tetrahedron Lett* 27:4051-4054 (1986); Froehler et al., *Nucl Acid Res* 14:5399-5407 (1986); Garegg et al., *Tetrahedron Lett* 27:4055-4058 (1986); Gaffney et al., *Tetrahedron Lett* 29:2619-2622 (1988)). These chemistries can be performed by a variety of automated oligonucleotide synthesizers available in the market.

20 The immunostimulatory nucleic acid may be any size of at least 6 nucleotides but in some embodiments are in the range of between 6 and 100 or in some embodiments between 8 and 35 nucleotides in size. Immunostimulatory nucleic acids can be produced on a large scale in plasmids. These may be administered in plasmid form or alternatively they can be degraded into oligonucleotides before administration.

25 A "stabilized immunostimulatory nucleic acid" shall mean a nucleic acid molecule that is relatively resistant to *in vivo* degradation (e.g., via an exo- or endo-nuclease). Stabilization can be a function of length or secondary structure. Nucleic acids that are tens to hundreds of kbs long are relatively resistant to *in vivo* degradation. For shorter nucleic acids, secondary structure can stabilize and increase their effect. For example, if the 3' end of an

oligonucleotide has self-complementarity to an upstream region, so that it can fold back and form a sort of stem loop structure, then the oligonucleotide becomes stabilized and therefore exhibits more activity.

Some stabilized immunostimulatory nucleic acids have a modified backbone. It has
5 been demonstrated that modification of the oligonucleotide backbone provides enhanced activity of the immunostimulatory nucleic acids when administered *in vivo*. Nucleic acids, including at least two phosphorothioate linkages at the 5' end of the oligonucleotide and multiple phosphorothioate linkages at the 3' end, preferably 5, may provide maximal activity and protect the oligonucleotide from degradation by intracellular exo- and endo-nucleases.
10 Other modified oligonucleotides include phosphodiester modified oligonucleotide, combinations of phosphodiester and phosphorothioate oligonucleotide, methylphosphonate, methylphosphorothioate, phosphorodithioate, and combinations thereof. Each of these combinations and their particular effects on immune cells is discussed in more detail in U.S. Pat. Nos. 6,194,388 and 6,207,646, the entire contents of which are incorporated herein by
15 reference. It is believed that these modified oligonucleotides may show more stimulatory activity due to enhanced nuclease resistance, increased cellular uptake, increased protein binding, and/or altered intracellular localization. Both phosphorothioate and phosphodiester nucleic acids are active in immune cells.

Other stabilized immunostimulatory nucleic acids include: nonionic DNA analogs,
20 such as alkyl- and aryl-phosphates (in which the charged phosphonate oxygen is replaced by an alkyl or aryl group), phosphodiester and alkylphosphotriesters, in which the charged oxygen moiety is alkylated. Oligonucleotides which contain diol, such as tetraethyleneglycol or hexaethyleneglycol, at either or both termini have also been shown to be substantially resistant to nuclease degradation.

25 Phosphorothioate nucleic acid molecules may be synthesized using automated techniques employing either phosphoramidate or H-phosphonate chemistries. Aryl- and alkyl-phosphonates can be made, e.g., as described in U.S. Pat. No. 4,469,863; and alkylphosphotriesters (in which the charged oxygen moiety is alkylated as described in U.S. Pat. No. 5,023,243 and European Patent No. 092,574) can be prepared by automated solid
30 phase synthesis using commercially available reagents. Methods for making other DNA backbone modifications and substitutions have been described. Uhlmann E and Peyman A (1990) *Chem Rev* 90:544; Goodchild J (1990) *Bioconjugate Chem* 1:165.

- 35 -

Other sources of immunostimulatory nucleic acids useful according to the invention include standard viral and bacterial vectors, many of which are commercially available. In its broadest sense, a "vector" is any nucleic acid material which is ordinarily used to deliver and facilitate the transfer of nucleic acids to cells. The vector as used herein may be an empty 5 vector or a vector carrying a gene which can be expressed. In the case when the vector is carrying a gene the vector generally transports the gene to the target cells with reduced degradation relative to the extent of degradation that would result in the absence of the vector. In this case the vector optionally includes gene expression sequences to enhance expression of the gene in target cells such as immune cells, but it is not required that the gene 10 be expressed in the cell.

Nucleic acid-binding fragments of TLRs are believed to include the extracytoplasmic (extracellular) domain or subportions thereof, such as those which include at least an MBD motif, a CXXC motif, or both an MBD motif and a CXXC motif.

Both mouse and human TLR9 have an N-terminal extension of approximately 180 15 amino acids compared to other TLRs. An insertion also occurs at amino acids 253-268, which is not found in TLRs 1-6 but is present in human TLR7 and human TLR8. This insert has two CXXC motifs which participate in forming a CXXC domain. The CXXC domain resembles a zinc finger motif and is found in DNA-binding proteins and in certain specific CpG binding proteins, e.g., methyl-CpG binding protein-1 (MBD-1). Fujita N et al. (2000) 20 *Mol Cell Biol* 20:5107-18. Both human and mouse TLR9 CXXC domains occur at aa 253-268:

CXXC motif:	GNCXXCXXXXXXCXXC	SEQ ID NO:62
Human TLR9:	GNCRRCDHAPNPCMEC	SEQ ID NO:63
25 Murine TLR9:	GNCRRCDHAPNPCMIC	SEQ ID NO:64

An additional motif believed to be involved in CpG binding is the MBD motif, also found in MBD-1, listed below as SEQ ID NO:53. Fujita, N et al. (2000) *Mol Cell Biol* 20:5107-18; Ohki I et al. (1999) *EMBO J* 18:6653-61. Amino acids 524-554 of hTLR9 and 30 aa 525-555 of mTLR9 correspond to the MBD motif of MBD-1 as shown:

MBD motif:

- 36 -

MBD-1	R-XXXXXXX-R-X-D-X-Y-XXXXXXXXXX-R-S-XXXXXX-Y	SEQ ID NO:65
hTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXXX-R-L-XXXXXX-Y	SEQ ID NO:66
mTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXXX-Q-L-XXXXXX-Y	SEQ ID NO:67
5	hTLR9 Q-VLDLSRN-K-L-D-L-Y-HEHSFTELP-R-L-EALDLS-Y	SEQ ID NO:68
	mTLR9 Q-VLDLSHN-K-L-D-L-Y-HWKSFSLEP-Q-L-QALDLS-Y	SEQ ID NO:69

Although the signaling functions of MBD-1 and TLR9 are quite different, the core D-X-Y is conserved and is believed to be involved in CpG binding.

10 According to another aspect of the invention, a screening method is provided for identifying an immunostimulatory compound. The method according to this aspect of the invention involves contacting a functional TLR9 with a test compound; detecting presence or absence of a response mediated by a TLR9 signal transduction pathway in the presence of the test compound arising as a result of an interaction between the functional TLR9 and the test compound; and determining the test compound is an immunostimulatory compound when the presence of a response mediated by the TLR9 signal transduction pathway is detected.

15 An immunostimulatory compound is a natural or synthetic compound that is capable of inducing an immune response when contacted with an immune cell. A TLR9 ligand that is an immunostimulatory compound is a natural or synthetic compound that is capable of inducing an immune response when contacted with an immune cell that expresses TLR9. A TLR9 ligand that is an immunostimulatory compound is also a natural or synthetic compound that is capable of inducing a TLR/IL-1R signal transduction pathway when contacted with a TLR9. Immunostimulatory compounds include but are not limited to immunostimulatory nucleic acids. The immunostimulatory compound can be, for example, a nucleic acid 20 molecule, polynucleotide or oligonucleotide, a polypeptide or oligopeptide, a lipid or 25 lipopolysaccharide, a small molecule.

20 A basis for certain of the screening assays is the presence of a functional TLR9 in a cell. The functional TLR9 in some instances is naturally expressed by a cell. In other instances, expression of the functional TLR9 can involve introduction or reconstitution of a 25 species-specific TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact with an

immunostimulatory nucleic acid. In yet other instances, expression of the functional TLR9 can involve introduction of a chimeric or modified TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact with an immunostimulatory nucleic acid. Examples of cell lines lacking TLR9 or immunostimulatory nucleic acid responsiveness include, but are not limited to, 293 fibroblasts (ATCC CRL-1573), MonoMac-6, THP-1, U937, CHO, and any TLR9 knock-out. The introduction of the species-specific, chimeric or modified TLR9 into the cell or cell line is preferably accomplished by transient or stable transfection of the cell or cell line with a TLR9-encoding nucleic acid sequence operatively linked to a gene expression sequence (as described above). Methods for transient and for stable transfection of a cell are well known in the art.

The screening assays can have any of a number of possible readout systems based upon either TLR/IL-1R signaling pathway or other assays useful for assessing response to immunostimulatory nucleic acids. It has been reported that immune cell activation by CpG immunostimulatory sequences is dependent in some way on endosomal processing.

In certain embodiments, the readout for the screening assay is based on the use of native genes or, alternatively, cotransfected or otherwise co-introduced reporter gene constructs which are responsive to the TLR/IL-1R signal transduction pathway involving MyD88, TRAF, p38, and/or ERK. Häcker H et al. (1999) *EMBO J* 18:6973-6982. These pathways activate kinases including κB kinase complex and c-Jun N-terminal kinases. Thus reporter genes and reporter gene constructs particularly useful for the assays can include a reporter gene operatively linked to a promoter sensitive to NF-κB. Examples of such promoters include, without limitation, those for NF-κB, IL-1 β , IL-6, IL-8, IL-12 p40, CD80, CD86, and TNF- α . The reporter gene operatively linked to the TLR-sensitive promoter can include, without limitation, an enzyme (e.g., luciferase, alkaline phosphatase, β -galactosidase, chloramphenicol acetyltransferase (CAT), etc.), a bioluminescence marker (e.g., green-fluorescent protein (GFP, U.S. Pat. No. 5,491,084), blue fluorescent protein, etc.), a surface-expressed molecule (e.g., CD25), and a secreted molecule (e.g., IL-8, IL-12 p40, TNF- α). In certain embodiments the reporter is selected from IL-8, TNF- α , NF-κB-luciferase (NF-κB-luc; Häcker H et al. (1999) *EMBO J* 18:6973-6982), IL-12 p40-luc (Murphy TL et al. (1995)

Mol Cell Biol 15:5258-5267), and TNF-luc (Häcker H et al. (1999) *EMBO J* 18:6973-6982). At least one of these reporter constructs (NF- κ B-luc) is commercially available (Stratagene, La Jolla, CA). In assays relying on enzyme activity readout, substrate can be supplied as part of the assay, and detection can involve measurement of chemiluminescence, fluorescence, 5 color development, incorporation of radioactive label, drug resistance, or other marker of enzyme activity. For assays relying on surface expression of a molecule, detection can be accomplished using FACS analysis or functional assays. Secreted molecules can be assayed using enzyme-linked immunosorbent assay (ELISA) or bioassays. Many such readout systems are well known in the art and are commercially available.

10 According to one embodiment of this method, comparison can be made to a reference immunostimulatory nucleic acid. The reference immunostimulatory nucleic acid may be any suitably selected immunostimulatory nucleic acid, including a CpG nucleic acid. In certain embodiments the screening method is performed using a plurality of test nucleic acids. In certain embodiments comparison of test and reference responses is based on comparison of 15 quantitative measurements of responses in each instance.

15 In another aspect the invention provides a screening method for identifying species specificity of an immunostimulatory nucleic acid. The method involves contacting a TLR9 of a first species with a test immunostimulatory nucleic acid; contacting a TLR9 of a second species with the test immunostimulatory nucleic acid; measuring a response mediated by a 20 TLR signal transduction pathway associated with the contacting the TLR9 of the first species with the test immunostimulatory nucleic acid; measuring a response mediated by the TLR signal transduction pathway associated with the contacting the TLR9 of the second species with the test immunostimulatory nucleic acid; and comparing the two responses. The TLR9 may be expressed by a cell or it may be part of a cell-free system. The TLR9 may be part of 25 a complex, with either another TLR or with another protein, e.g., MyD88, IRAK, TRAF, I κ B, NF- κ B, or functional homologues and derivatives thereof. Thus for example a given ODN can be tested against a panel of human fibroblast 293 fibroblast cells transfected with TLR9 from various species and optionally cotransfected with a reporter construct sensitive to TLR/IL-1R activation pathways. Thus in another aspect, the invention provides a method for 30 screening species selectivity with respect to a given nucleic acid sequence.

Test compounds can include but are not limited to peptide nucleic acids (PNAs), antibodies, polypeptides, carbohydrates, lipids, hormones, and small molecules. Test

- 39 -

compounds can further include variants of a reference immunostimulatory nucleic acid incorporating any one or combination of the substitutions described above. Test compounds can be generated as members of a combinatorial library of compounds.

In preferred embodiments, the screening methods can be performed on a large scale and with high throughput by incorporating, e.g., an array-based assay system and at least one automated or semi-automated step. For example, the assays can be set up using multiple-well plates in which cells are dispensed in individual wells and reagents are added in a systematic manner using a multiwell delivery device suited to the geometry of the multiwell plate. Manual and robotic multiwell delivery devices suitable for use in a high throughput screening assay are well known by those skilled in the art. Each well or array element can be mapped in a one-to-one manner to a particular test condition, such as the test compound. Readouts can also be performed in this multiwell array, preferably using a multiwell plate reader device or the like. Examples of such devices are well known in the art and are available through commercial sources. Sample and reagent handling can be automated to further enhance the throughput capacity of the screening assay, such that dozens, hundreds, thousands, or even millions of parallel assays can be performed in a day or in a week. Fully robotic systems are known in the art for applications such as generation and analysis of combinatorial libraries of synthetic compounds. See, for example, U.S. Pat. Nos. 5,443,791 and 5,708,158.

The following examples are provided for illustrative purposes and are not meant to be limiting in any way.

Examples

Example 1. Cloning and Sequencing of Rat, Porcine, Bovine, Equine, Ovine, Canine, and Feline TLR9

Cells and Tissues. Lymphoid tissues, primarily spleen or blood mononuclear cells (PBMC) from five mammalian species were collected: mouse, pig, bovine, rat and horse. Spleen samples were collected in RNAlater™ (Ambion®, Austin, TX, USA), stabilized at 4°C overnight and stored at -70°C. Blood samples were centrifuged at 500 x g for 25 min at room temperature and the buffy coat, containing enriched PBMC, was then removed and stored at -70°C. The mouse specimen was used as a comparative positive control.

- 40 -

First-strand cDNA synthesis. Total RNA from the spleen and PBMC samples was isolated using a monophasic solution of phenol and guanidine isothiocyanate: TRIzolTM reagent (GIBCO BRL[®], Burlington, ON, Canada) according to the manufacturer's instructions. First-strand cDNA was synthesized from the total RNA using 5 SUPERSCRIPTTM II reverse transcriptase (GIBCO BRL[®], Burlington, ON, Canada). Approximately 3 µg of total RNA was added to 50 pmoles of oligo(dT) primer [poly T₍₁₈₎]; the mixture was heated to 70°C for 10 min and subsequently chilled on ice. The following was added to the cooled reaction mixture: 1 µl of mixed dNTP stock containing 10 mM each dATP, dCTP, dGTP and dTTP (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) at 10 neutral pH, 1X first strand buffer (50 mM Tris-HCl pH 8.3/ 75 mM KCl/ 3 mM MgCl₂) and 2 µl of 0.1 M DTT. The mixture was subsequently heated to 42°C for 2 min, followed by addition of 200 units of SUPERSCRIPTTM II reverse transcriptase. The reaction was carried out at 42°C for 50 min, followed by 70°C for 15 min. The first-strand cDNA was used as the template for subsequent polymerase chain reaction (PCR) amplifications.

15 *PCR amplification.* TLR9 gene was PCR amplified from each of the above-mentioned species using primers designed from known mouse and human TLR9 sequence in Genbank: Accession AF314224 and AF259262, respectively. The primers were designed using the primer design software, Clone Manager 5 (Scientific and Educational Software, Durham, NC, USA). TLR9 gene-specific primers used were:
20 forward primer 5'-ACCTTGCCTGCCTTCCTACCCTGTGA-3' (SEQ ID NO:37) and reverse primer 5'-GTCCGTGTGGGCCAGCACAAA-3' (SEQ ID NO:38). The 2.7 Kbp fragment was PCR amplified using Advantage[®] 2 DNA polymerase mix (BD Biosciences Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. PCR reaction volumes of 25 µl contained 15 pmoles of each primer, 0.2 mM of dNTP mix 25 and 1 µl of reverse transcription reaction. PCR amplification was conducted by initial denaturation at 94°C for 1 min followed by 30 cycles of 94°C denaturation (15 sec), 65°C annealing (45 sec) and 72°C extensions (2 min), with a final extension at 72°C for 5 min.

30 *Cloning and sequencing.* The PCR amplified fragment was treated with 500 units of T4 DNA polymerase (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) for 15 min at room temperature prior to cleaning the reaction with QIAquick PCR purification kit (QIAGEN Inc., Mississauga, ON, Canada). The fragment was then ligated to pZErOTM - 2

- 41 -

vector (Invitrogen™ Life Technologies, Burlington, ON, Canada), treated with *Eco RV* restriction enzyme, using T4 DNA Ligase (GIBCO BRL®, Burlington, ON, Canada). *E. coli* TOP 10 chemically competent cells (Invitrogen™ Life Technologies, Burlington, ON, Canada) were used to transform ligated products. Plasmids containing the 2.7 Kbp fragment 5 were sequenced using an automated DNA sequencer, CEQ™ 2000XL DNA analysis system (Beckman Coulter Inc., Fullerton, CA, USA).

Sequences of the 2.7 Kbp fragment were derived from three clones of each species selected from independent PCR reactions to account for errors that may have been incurred during the PCR amplifications and to confirm the sequence data.

10 Nucleotide sequences of the rat, porcine, bovine, equine, ovine, canine, and feline TLR9 were extended and completed using standard 5' and 3' RACE PCR and primers designed using the sequences obtained from the 2.7 Kbp fragments.

15 *Results.* Nucleotide sequences of rat, porcine, bovine, equine, canine, and feline TLR9 cDNA obtained by the methods above are provided as SEQ ID NOs 3, 7, 11, 15, 19, 23, and 27, respectively. Dduced amino acid sequences are provided as SEQ ID NOs 1, 5, 9, 13, 17, 21, and 25, respectively. Dduced amino acid sequences of full-length murine and human TLR9 are provided as SEQ ID NOs 29 and 33, respectively.

Example 2. Comparison of Aligned Sequences for TLR9 from Various Mammalian Species.

20 Multiple sequence alignment of deduced amino acid sequences for feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 polypeptides was performed using Clustal W 1.82 (see, for example, www.cmbi.kun.nl/bioinf/tools/clustalw.shtml). In addition, paired sequence alignment of deduced amino acid sequences for murine and human TLR9 polypeptides was performed using Clustal W 1.82. The results of the multiple 25 sequence alignment are presented in **Figure 1**. As will be appreciated from Figure 1, certain amino acids are highly conserved across all species examined. Similarly, certain amino acids differ only by conservative amino acid substitutions among the various species. In addition, it is evident that certain amino acids which are conserved between murine and human TLR9 30 are not conserved in other species. Furthermore, Figure 1 also indicates that certain amino acids are highly divergent across various species. The information provided by the comparison of multiple species adds significantly to the information available by comparison between only murine and human TLR9 sequences.

- 42 -

The putative transmembrane regions of the TLR9 polypeptides are indicated in boxes in Figure 1. Sequence upstream of each transmembrane region is extracellular domain and is believed to include sequence primarily responsible for binding to TLR9 ligands, including CpG DNA. The extracellular domains of feline, canine, bovine, mouse, ovine, porcine, 5 horse, human, and rat TLR9 correspond to amino acids numbered 1-820, 1-822, 1-818, 1-821, 1-818, 1-819, 1-820, 1-820, and 1-821, respectively, as shown in Figure 1.

Figure 2 presents an evolutionary relatedness tree for six TLR9 polypeptides examined. The cladogram in Figure 2 was prepared using Clustal W (see above). As can be appreciated from this figure, murine and human TLR9 are nearly the most divergent TLR9s 10 in this group. Surprisingly, human and horse TLR9 appear relatively closely related.

Example 3. Reconstitution of TLR9 Signaling in 293 Fibroblasts.

Mouse TLR9 cDNA (SEQ ID NO:31) and human TLR9 cDNA (SEQ ID NO:35) in pT-Adv vector (from Clonetech) were individually cloned into the expression vector 15 pcDNA3.1(-) from Invitrogen using the EcoRI site. Utilizing a "gain of function" assay it was possible to reconstitute human TLR9 (hTLR9) and murine TLR9 (mTLR9) signaling in CpG-DNA non-responsive human 293 fibroblasts (ATCC, CRL-1573). The expression vectors mentioned above were transfected into 293 fibroblast cells using the calcium phosphate method.

20 Since NF- κ B activation is central to the IL-1/TLR signal transduction pathway (Medzhitov R et al. (1998) *Mol Cell* 2:253-258; Muzio M et al. (1998) *J Exp Med* 187:2097-101), cells were transfected with hTLR9 or co-transfected with hTLR9 and an NF- κ B-driven luciferase reporter construct. Human fibroblast 293 cells were transiently transfected with hTLR9 and a six-times NF- κ B-luciferase reporter plasmid (NF- κ B-luc) or with hTLR9 alone. 25 After stimulus with CpG-ODN (2006, 2 μ M, TCGTCGTTTGTCGTTTGTCGTT, SEQ ID NO:58), GpC-ODN (2006-GC, 2 μ M, TGCTGCTTGTGCTTTGTGCTT, SEQ ID NO:59), LPS (100 ng/ml) or media, NF- κ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results representative of three independent experiments showed that cells expressing hTLR9 responded to CpG-DNA but not to LPS.

30 Independently, human fibroblast 293 cells were transiently transfected with mTLR9 and the NF- κ B-luc construct or with mTLR9 alone. After stimulation with CpG-ODN (1668, 2 μ M; TCCATGACGTTCTGATGCT, SEQ ID NO:60), GpC-ODN (1668-GC, 2 μ M;

- 43 -

TCCATGAGCTTCCTGATGCT, SEQ ID NO:61), LPS (100 ng/ml) or media, NF- κ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results showed that expression of TLR9 (human or mouse) in 293 cells results in a gain of function for CpG-DNA stimulation.

5 To generate stable clones expressing human TLR9, murine TLR9, or either TLR9 with the NF- κ B-luc reporter plasmid, 293 cells were transfected in 10 cm plates (2×10^6 cells/plate) with 16 μ g of DNA and selected with 0.7 mg/ml G418 (PAA Laboratories GmbH, Cölbe, Germany). Clones were tested for TLR9 expression by RT-PCR. The clones were also screened for IL-8 production or NF- κ B-luciferase activity after stimulation with
10 ODN. Four different types of clones were generated.

15 293-hTLR9-luc: expressing human TLR9 and 6-fold NF- κ B-luciferase reporter
293-mTLR9-luc: expressing murine TLR9 and 6-fold NF- κ B-luciferase reporter
293-hTLR9: expressing human TLR9
293-mTLR9: expressing murine TLR9

Results indicated that stable clones also responded to CpG-ODN.

Example 4. Similar ODN Sequence Specificity of TLR9 of Human and Equine TLR9.

20 3×10^6 293T cells were electroporated with 5 μ g NF- κ B-luc plasmid and 5 μ g of either horse TLR9-pcDNA3.1 plasmid or human TLR9-pcDNA3.1 plasmid at 200V, 975 μ F. After the electroporation the cells were plated in 96-well cell culture plates at 2.5×10^4 cells per well and grown overnight at 37°C. The cells were stimulated with the indicated concentration of ODN for 16h, after which the supernatant was removed and the cells lysed in lysis buffer and
25 frozen for at least 2 hours at -80°C. Luciferase activity was measured by adding Luciferase Assay substrate from Promega. Values are given as fold specific induction over non-stimulated control. Results are shown in Figure 3.

As shown in Figure 3, ODN 2006 (TCGTCGTTTGTCTCGTTTGTCTGTT; SEQ ID NO:58) has a strong specificity for human TLR9. ODN 1982 (TCCAGGACTTCTCTCAGGTT; SEQ ID NO:70) was the negative control ODN. ODN 5890 (TCCATGACGTTTGATGTT; SEQ ID NO:39) has a strong specificity for mouse

- 44 -

TLR9. This experiment demonstrates the similarity of horse TLR9 to human TLR9 in binding specificity, a result predicted by the evolutionary relatedness of horse TLR9 to human TLR9. Mouse TLR9 is more distant from horse TLR9 and human TLR9 in sequence homology, and ODN 5890 was not detected by either human or horse TLR9.

5

Example 5. Non-human, Non-murine Native Mammalian TLR9 Useful in Screening for Human-Preferred CpG DNA.

Native rat, porcine, bovine, equine, and ovine TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 10 2006). Rat, porcine, bovine, equine, or ovine TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The 15 cells expressing the selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

20 Example 6. Chimeric TLR9 Useful in Screening for Human-Preferred CpG DNA.

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector 25 containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

30

Example 7. Chimeric TLR9 Responsive to Both Human-Preferred and Murine-Preferred CpG DNA.

- 45 -

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006) and also screened for binding or TLR9 signaling activity when contacted with murine-preferred CpG DNA (ODN 1668). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling

5 activity in each of these assays are then used as the basis for screening for additional human-preferred CpG DNA and for screening for additional murine-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with

10 candidate human-preferred CpG DNA or candidate murine-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA. Candidate murine-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as murine-preferred CpG DNA.

15

Equivalents

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by examples provided, since the examples are intended as a single illustration of one aspect of

20 the invention and other functionally equivalent embodiments are within the scope of the invention. Various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims. The advantages of the invention are not necessarily encompassed by each embodiment of the invention.

25 All references, patents and patent publications that are recited in this application are incorporated in their entirety herein by reference.

We claim:

Claims

1. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.

5

2. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.

3. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a 10 polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.

4. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a 15 polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.

5. A vector comprising the nucleic acid of any of claims 3-4.

6. A cell comprising the vector of claim 5.

20

7. An antibody or fragment thereof that binds specifically to the polypeptide of any of claims 1-2.

8. A method for identifying key amino acids in a TLR9 of a first species which 25 confer specificity for CpG DNA optimized for TLR9 of the first species, comprising:

aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species;

30 generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the

- 47 -

TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with 5 the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

10 9. A method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9, comprising:

aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a 15 CpG DNA optimized for murine TLR9;

generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the 20 initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids.

25

10. The method according to claim 9, performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight, said weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred 30 CpG DNA).

11. An isolated polypeptide comprising an amino acid sequence identical to SEQ ID NO:30 except for substitution of at least one key amino acid identified according to the method of any of claims 9 or 10.

5 12. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide according to claim 11.

13. A vector comprising the nucleic acid of claim 12.

10 14. A cell comprising the vector of claim 13.

15. An antibody that binds specifically to the polypeptide of claim 14.

16. A screening method to identify a TLR9 ligand, comprising:
15 contacting a polypeptide according to any of claims 1, 2, or 11 with a candidate TLR9 ligand;
measuring a signal in response to the contacting; and
identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling.

20 17. The method of claim 16, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

25 18. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF-κB.

19. The method of claim 17, wherein the candidate TLR9 ligand is an immunostimulatory nucleic acid.

30 20. The method of claim 19, wherein the immunostimulatory nucleic acid is CpG DNA.

- 49 -

21. A screening method to identify species-specific CpG-motif preference of an isolated polypeptide of claim 2 or claim 11, comprising:

contacting an isolated polypeptide of claim 2 or claim 11 with a CpG DNA comprising a hexamer sequence selected from the group consisting of GACGTT, AACGTT, 5 CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG;

measuring a signal in response to the contacting; and

10 identifying a species-specific CpG-motif preference when the signal in response to the contacting is consistent with TLR9 signaling.

22. The method of claim 21, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

15 23. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF- κ B.

24. The method of claim 21, wherein the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

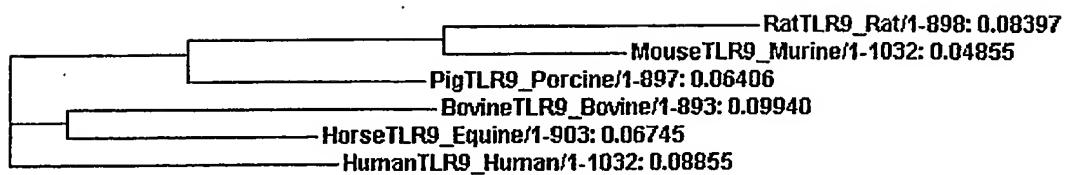
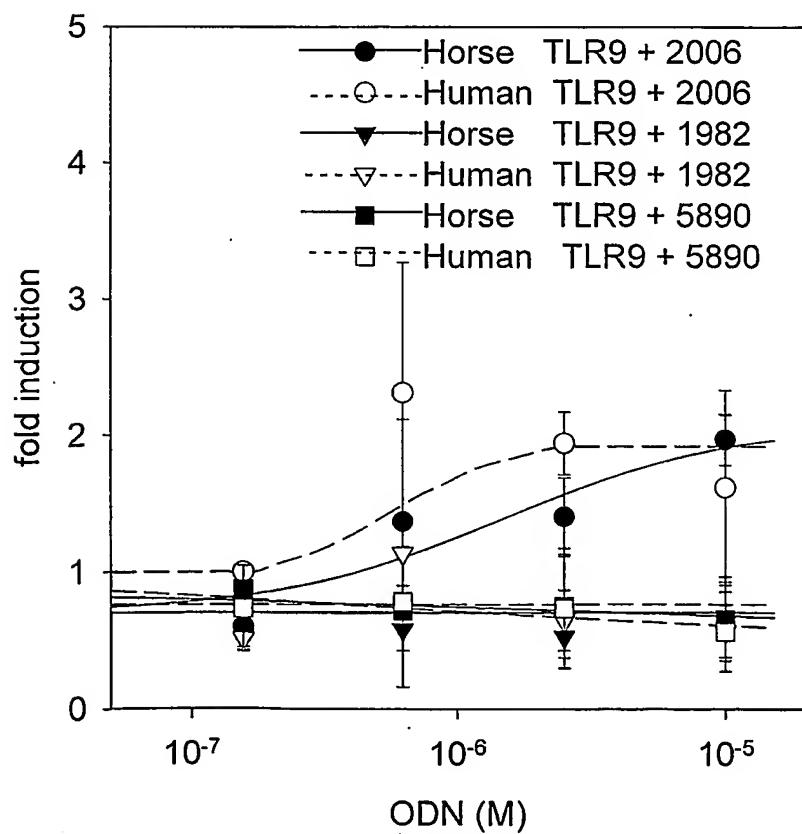
20 TCCATGACGTTTGATGTT (SEQ ID NO:39),
TCCATAACGTTTGATGTT (SEQ ID NO:40),
TCCATCACGTTTGATGTT (SEQ ID NO:41),
TCCATTACGTTTGATGTT (SEQ ID NO:42),
TCCATGGCGTTTGATGTT (SEQ ID NO:43),
25 TCCATGCCGTTTGATGTT (SEQ ID NO:44),
TCCATGTCGTTTGATGTT (SEQ ID NO:45),
TCCATGATGTTTGATGTT (SEQ ID NO:46),
TCCATGAAGTTTGATGTT (SEQ ID NO:47),
TCCATGAGGTTTGATGTT (SEQ ID NO:48),
30 TCCATGACATTTGATGTT (SEQ ID NO:49),
TCCATGACCTTTGATGTT (SEQ ID NO:50),
TCCATGACTTTGATGTT (SEQ ID NO:51),
TCCATGACGCTTGATGTT (SEQ ID NO:52),
TCCATGACGATTGATGTT (SEQ ID NO:53),
35 TCCATGACGGTTTGATGTT (SEQ ID NO:54),
TCCATGACGTTGATGTT (SEQ ID NO:55),
TCCATGACGTATTGATGTT (SEQ ID NO:56), and
TCCATGACGTGTTGATGTT (SEQ ID NO:57).

Figure 1
(1/3)

Figure 1
(2/3)

Figure 1
(3/3)

canine	LEDRKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1016
bovine	LEDRKDVVVLVILCPDAHRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1018
mouse	LEDRKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1014
ovine	LEDRKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1014
porcine	LEDRKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1014
horse	LEDRKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1015
human	LEDRKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1016
rat	LEDRKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1018
	*****	*****
canine	HFYNQNFCRGPTTAE-----	1031
bovine	HFYNQNFCRGPTTAE-----	1032
mouse	HFYNRNFCRGPTTAE-----	1029
ovine	HFYNRNFCRGPTTAE-----	1032
porcine	HFYNRNFCRGPTTAE-----	1029
horse	HFYNRNFCRGPTTAE-----	1030
human	HFYNRNFCRGPTTAE-----	1031
rat	HFYNRNFCRGPTTAE-----	1032
	*****	*****
canine	CGWDLWYCFHLCIAWLPLRRGRR--RGADALPYDAFVVFDKAQS	896
bovine	CGWDLWYCFHLCIAWLPLRRGRR--RGVDALAYDAFVVFDKAQS	898
mouse	CGWDLWYCFHLCIAHLPLRRRQ--RGEDTLLYDAVVVFDKVQS	894
ovine	CGWDLWYCFHLCIAHLPLRRRQ--RGEDTLLYDAVVVFDKVQS	894
porcine	CGWDLWYCFHLCIAHLPLRRRQ--RGEDTLLYDAVVVFDKVQS	894
horse	CGWDLWYCFHLCIAHLPLRRRQ--RGADALFYDAFVVFDKAQS	895
human	CGWDLWYCFHLCIAHLPLRRRQ--RGADALSYDAFVVFDKAQS	896
rat	CGWDLWYCFHLCIAHLPLRRRQ--RGADALYDAFVVFDKAQS	898
	*****	*****
canine	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMFLVLAHTD	956
bovine	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMFLVLAHTD	958
mouse	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMFLVLAHTD	954
ovine	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMFLVLAHTD	954
porcine	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMFLVLAHTD	954
horse	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMFLVLAHTD	955
human	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMFLVLAHTD	956
rat	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMFLVLAHTD	958
	*****	*****
canine	LEDRKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1016
bovine	LEDRKDVVVLVILCPDAHRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1018
mouse	LEDRKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1014
ovine	LEDRKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1014
porcine	LEDRKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1014
horse	LEDRKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1015
human	LEDRKDVVVLVILSPDARRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1016
rat	LEDRKDVVVLVILSPDARRSRYVRLRQRLCRQSVLLWPHQPSGQRFWAQLGTALTRDNQ	1018
	*****	*****
canine	HFYNQNFCRGPTTAE-----	1031
bovine	HFYNQNFCRGPTTAE-----	1032
mouse	HFYNRNFCRGPTTAE-----	1029
ovine	HFYNRNFCRGPTTAE-----	1032
porcine	HFYNRNFCRGPTTAE-----	1029
horse	HFYNRNFCRGPTTAE-----	1030
human	HFYNRNFCRGPTTAE-----	1031
rat	HFYNRNFCRGPTTAE-----	1032
	*****	*****

Figure 2**Figure 3**

SEQUENCE LISTING

<110> Coley Pharmaceutical GmbH
University of Saskatchewan
Qiagen GmbH

<120> TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

<130> C1041.70040W000

<150> US 60/412,479
<151> 2002-09-19

<160> 70

<170> PatentIn version 3.1

<210> 1
<211> 1032
<212> PRT
<213> Rattus norvegicus

<400> 1

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn
50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn
65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met
100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130 135 140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro
180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser
260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe
290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu
325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala
340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu
355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu
370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala
405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr
420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val
435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser
450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu
465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp
515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser
565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val
580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly
595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe

610 615 620

Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu
645 650 655

Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser
660 665 670

Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn
675 680 685

Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
740 745 750

Leu Thr Val Leu Asp Val Ser Ser Asn Pro Leu His Cys Ala Cys Gly
755 760 765

Ala Pro Phe Val Asp Leu Leu Glu Val Gln Thr Lys Val Pro Gly
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Arg Gln Leu Gln Gly Arg
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Asp Val Leu Ser
805 810 815

Arg Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Thr Val
820 825 830

Leu Pro Leu Leu Gln His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe
835 840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Thr Arg Gly Arg Arg Ser
850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu
885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp
900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Lys Val Ser
930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
980 985 990

Leu Phe Trp Pro His Gln Pro Asn Gly Gln Gly Ser Phe Trp Ala Gln
995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg
1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu
1025 1030

<210> 2
<211> 821
<212> PRT
<213> Rattus norvegicus

<400> 2

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn
50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn
65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met
100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130 135 140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro
180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser
260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe
290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu
325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala
340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu
355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu
370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala
405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr
420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val
435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser
450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu
465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp
515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser
565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val
580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly
595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe
610 615 620

Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu
645 650 655

Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser
660 665 670

Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn
675 680 685

Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn

725

730

735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
 740 745 750

Leu Thr Val Leu Asp Val Ser Ser Asn Pro Leu His Cys Ala Cys Gly
 755 760 765

Ala Pro Phe Val Asp Leu Leu Glu Val Gln Thr Lys Val Pro Gly
 770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Arg Gln Leu Gln Gly Arg
 785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Asp Val Leu Ser
 805 810 815

Arg Asp Cys Phe Gly
 820

<210> 3
 <211> 3099
 <212> DNA
 <213> Rattus norvegicus

<400> 3
 atggttctct gtcgcaggac cctgcacccc ttgtctctcc tggcacaggc cgcaatgcgt 60
 gctgaggctc tggccctggg taccctgcct gccttcctac cctgtgaact gaaggctcat 120
 ggcctggtag actgcaactg gctcttcctg aagtctgtgc ctcacttctc tgccgcagaa 180
 ccccggttcca acatcaccag ctttccttg atcgccaaacc gcatccacca cctgcacaac 240
 ctcgactttg tccacctgca caacgtgcga cagctgaacc tcaagtggaa ctgtccgc 300
 cctggcctca gccccttgccttgc cgcacatgacca ttgagccaa aaccttcctg 360
 gctatgcga tgctggaaaga gctgaacctg agctataacg gtatcaccac tggcccccgc 420
 ctgcccagct ccctgacgaa tctgaggcta agccacacca acatcctggt actcgatgcc 480
 agcagcctcg ctggcctgca cagcctgcga gttctttca tggacggaa ctgtactac 540
 aagaacccct gcaacggggc ggtgaacgtg accccggacg ctttcctggg cttgagcaac 600
 ctcacccact tggcccttaa gtataacaac ctcacagagg tggcccgcca actgcccccc 660
 agcctggagt acctcctgct gtcctataac ctcatgtca agctggggc cgaagaccta 720
 gccaacctga ctcacccatcg aatgcttgat tgggtggga attgcccgtcg ctgtgatcac 780

gcccccgacc	tctgtacaga	atgccggcag	aagtcccctg	atctgcaccc	tcagactttc	840
catcacctga	gccaccttga	aggcctggt	ctgaaggaca	gttctctcca	ctcgctgaac	900
tccaaagtgg	tccagggtct	ggcgaacctc	tcggtgctgg	acctaagcga	gaactttctc	960
tacgagagca	tcaacaaaac	cagcgcctt	cagaacctga	cccgtctgca	caagctcgac	1020
ctgtccttca	attactgcaa	gaaggtatcg	ttcgcccccc	tccacctggc	aagttccttc	1080
aagagcctgg	tgtcgctgca	ggagctgaac	atgaacggca	tcttcttccg	cttactcaac	1140
aagaacacgc	tcaggtggct	ggctggctcg	cccaagctcc	acacgctgca	ccttcaaatg	1200
aatttcatca	accaggcgca	gctcagcgtc	tttagtacct	tccgagccct	tcgctttgtg	1260
gacctgtcca	ataatcgcat	cagcggccct	ccaaacgtgt	ccagagtcgc	ccccgaaaag	1320
gcagacgagg	cggagaaggg	ggttccatgg	cctgcaagtc	tcaccccaagc	tctcccagc	1380
actcccgct	caaagaactt	catggtcagg	tgttagaacc	tcagattcac	catggacactg	1440
tctcggaaaca	accaggtgac	tatcaagcca	gagatgttcg	tcaacctctc	ccatctccag	1500
tgtctgagcc	tgagccacaa	ctgcatcgcg	caggctgtca	atggctctca	gttcctgccc	1560
ctgaccaacc	tgaaggtgct	ggacctgtcc	tataacaagc	tggacctgta	ccattcgaaa	1620
tcgttcagt	agctcccaca	gttgcaggcc	ctggacctga	gctacaacag	ccagccattc	1680
agcatgcagg	ggataggcca	caacttcagt	tttctggcca	atctgtccag	gttacagaac	1740
cttagcctgg	cacacaatga	cattcacagc	cgcggtgtcct	cacgcctcta	cagcacctca	1800
gtggagtatc	tggacttcag	cggcaacgg	gtggggccgca	tgtgggacga	ggaggacctt	1860
tacctctatt	tcttccaaga	cctgagaagc	ctgattcatc	tggacctgta	tcagaataag	1920
ctgcacatcc	tccggccccca	gaacctcaac	tacctccccca	agagcctgac	gaagctgagt	1980
ttccgtgaca	atcacctctc	tttctttaac	tggagcagtc	tggccttcct	gcccaatctg	2040
cgagacctgg	acctggcagg	caatctacta	aaggccctga	ccaaacggcac	cctgcctaatt	2100
ggcacgctcc	tccagaaact	ggatgtcagt	agcaacagta	tcgtctttgt	ggtcccagcc	2160
ttctttgttc	tggcggtaga	gctaaaagag	gtcaacctca	gccataacat	cctcaagact	2220
gtggatcgat	cctgggtttgg	gcccatgt	atgaacctga	cggttctaga	cgtgagcagc	2280
aaccctctgc	attgtgcctg	cggtgacacc	ttttagact	tactgctgga	agtgcagacc	2340
aaggtgcctg	gcctggctaa	cggtgtgaag	tgtggcagtc	ccggccagct	gcagggccgc	2400
agcatctttg	cgcaagaccc	gcggctgtgc	ctggatgacg	tcctttctcg	ggactgcttt	2460
ggcctttcac	tcctggctgt	ggccgtgggc	acggtgttgc	ctttactgca	gcatctctgc	2520
ggctgggacg	tctggtaactg	tttccatctg	tgcctggcat	ggctaccctt	gctgaccctgt	2580

ggccggcgca	gcccggca	gcccggca	tctcccttat	gatgccttcg	tggtgttcga	taaggcgcag	2640
agcgcgggtt	ctgactgggt	gtataacgag	cttcgagtgc	ggctagagga	gcggcgcgg	gt	2700
cgccgagccc	tacgcttgtg	tctggaggac	cgagattggc	tgcctggcca	gacactcttc		2760
gagaacctct	gggcctccat	ctatggcagc	cgcaagactc	tgtttgtgct	ggcccacacg		2820
gacaaggta	gtggcctcct	gcccggcc	ttcctgctgg	ctcagcagcg	cctgctggag		2880
gaccgcaagg	acgtggtggt	gttggtgatc	ctgcgcctg	atgcccacccg	ctcccgctac		2940
gtgcactgc	gccagcgcct	ctgcccag	agtgtgctct	tctggcccca	tcagcccaac		3000
gggcagggca	gcttctgggc	ccagctgagt	acagccctga	ctagggacaa	ccaccacttc		3060
tataaccgga	acttctgccc	gggacactaca	gcagaatag				3099

<210> 4
 <211> 2463
 <212> DNA
 <213> Rattus norvegicus

<400> 4	atgggttctct	gtcgaggac	cctgcacccc	ttgtctctcc	tggcacaggc	cgcaagtgc	60
	gctgaggctc	tggccctggg	taccctgcct	gccttcctac	cctgtgaact	gaaggcctcat	120
	ggcctggtag	actgcaactg	gtcttcctg	aagtctgtgc	ctcacttctc	tgccgcagaa	180
	ccccgttcca	acatcaccag	ccttccttg	atcgccaacc	gcatccacca	cctgcacaac	240
	ctcgactttg	tccacctgcc	caacgtgcga	cagctgaacc	tcaagtggaa	ctgtccgccc	300
	cctggcctca	gccccttgca	cttctcctgc	cgcacatgacca	ttgagccaa	aaccttcctg	360
	gctatgcgca	tgctggaaga	gctgaacctg	agctataacg	gtatcaccac	tgtccccgc	420
	ctgcccagct	ccctgacgaa	tctgaggcta	agccacacca	acatcctggt	actcgatgcc	480
	agcagcctcg	ctggcctgca	cagcctgcga	gttctttca	tggacggaa	ctgctactac	540
	aagaacccct	gcaacggggc	ggtgaacgtg	accccgacg	cttcctggg	ctttagcaac	600
	ctcacccact	tgtcccttaa	gtataacaac	ctcacagagg	tgcggccca	actgcccccc	660
	agcctggagt	acctcctgct	gtcctataac	ctcatcgta	agctggggc	cgaaagaccta	720
	gccaacctga	cctcccttcg	aatgcttgat	gtgggtggga	attgcccgtcg	ctgtgatcac	780
	gccccggacc	tctgtacaga	atgcccggcag	aagtcccttg	atctgcaccc	tcaagactttc	840
	catcacctga	gccacccctga	aggcctggtg	ctgaaggaca	gttctctcca	ctcgctgaac	900
	tccaagtgg	tccagggtct	ggcgaacctc	tcggtgctgg	acctaagcga	gaactttctc	960
	tacgagagca	tcaacaaaac	cagcgccttt	cagaacctga	cccgtctgcg	caagctcgac	1020

ctgtccttca	attactgcaa	gaaggtatcg	ttcgcccgcc	tccacctggc	aagttccttc	1080
aagagcctgg	tgtcgctgca	ggagctgaac	atgaacggca	tcttcttccg	cttactcaac	1140
aagaacacgc	tcaggtggct	ggctggctcg	cccaagctcc	acacgctgca	ccttcaaatg	1200
aatttcatca	accaggcgca	gctcagcgtc	tttagtacct	tccgagccct	tcgctttgtg	1260
gacctgtcca	ataatcgcat	cagcgggct	ccaacgctgt	ccagagtgc	ccccgaaaag	1320
gcagacgagg	cggagaaggg	ggttccatgg	cctgcaagtc	tcaccccagc	tctcccgagc	1380
actcccgct	caaagaactt	catggtcagg	tgttagaacc	tcagattcac	catggacctg	1440
tctcggaca	accaggtgac	tatcaagcca	gagatgttcg	tcaacctctc	ccatctccag	1500
tgtctgagcc	tgagccacaa	ctgcacatcg	caggctgtca	atggctctca	gttcctgccc	1560
ctgaccaacc	tgaaggtgct	ggacctgtcc	tataacaagc	tggacctgtta	ccattcgaaa	1620
tcgttcagtg	agctcccaca	gttgcaggcc	ctggacctga	gctacaacag	ccagccattc	1680
agcatgcagg	ggataggcca	caacttcagt	tttctggcca	atctgtccag	gttacagaac	1740
cttagcctgg	cacacaatga	cattcacagc	cgcgtgtcct	cacgcctcta	cagcacctca	1800
gtggagtatc	tggacttcag	cggcaacgg	gtggggccgca	tgtgggacga	ggaggacctt	1860
tacctctatt	tcttccaaga	cctgagaagc	ctgattcatc	tggacctgtc	tcagaataag	1920
ctgcacatcc	tccggccccca	gaacctcaac	tacctccccca	agagcctgac	gaagctgagt	1980
ttccgtgaca	atcacctctc	tttcttaac	tggagcagtc	tggccttcct	gcccaatctg	2040
cgagacctgg	acctggcagg	caatctacta	aaggccctga	ccaacggcac	cctgcctaatt	2100
ggcacgtcc	tccagaaact	ggatgtcagt	agcaacagta	tgcgtttgt	ggtcccagcc	2160
ttctttgctc	tggcggtaga	gctaaaagag	gtcaacctca	gccataacat	cctcaagact	2220
gtggatcgct	cctgggttg	gcccattgtg	atgaacctga	cggttctaga	cgtgagcagc	2280
aaccctctgc	attgtgcctg	cggtgacacc	ttttagact	tactgctgga	agtgcagacc	2340
aaggtgcctg	gcctggctaa	cggtgtgaag	tgtggcagtc	cccgccagct	gcagggccgc	2400
agcattttg	cgcaagacct	gcggctgtgc	ctggatgacg	tcctttctcg	ggactgcttt	2460
ggc						2463

1

<210> 5
 <211> 1030
 <212> PRT
 <213> *Sus scrofa*

<400> 5

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val
1 5 10 15

Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr
145 150 155 160

His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu
210 215 220 225

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro
260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg
290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
305 310 315 320

Asp Cys Ile Thr Lys Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg
325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln
370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn
385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu
405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro
435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp
450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg
465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg
485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn
500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser
515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro
530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met
545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu
565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln
580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp
595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln
610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His
625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His
645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu
660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu
675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg
690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe

705	710	715	720
Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu			
725	730	735	
Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys			
740	745	750	
Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr			
755	760	765	
Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro			
770	775	780	
Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile			
785	790	795	800
Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn			
805	810	815	
Cys Phe Gly Ile Ser Leu Leu Ala Met Ala Leu Gly Leu Val Val Pro			
820	825	830	
Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu			
835	840	845	
Cys Leu Ala Trp Leu Pro His Arg Gly Gln Arg Arg Gly Ala Asp Ala			
850	855	860	
Leu Phe Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val			
865	870	875	880
Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg			
885	890	895	
Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro			
900	905	910	
Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg			
915	920	925	
Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu			
930	935	940	

Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys
 945 950 955 960

Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala Tyr Arg Ser Arg
 965 970 975

Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp
 980 985 990

Pro His Gln Pro Arg Gly Gln Gly Ser Phe Trp Ala Gln Leu Gly Thr
 995 1000 1005

Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg Asn Phe Cys
 1010 1015 1020

Arg Gly Pro Thr Thr Ala Glu
 1025 1030

<210> 6
 <211> 819
 <212> PRT
 <213> Sus scrofa

<400> 6

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val
 1 5 10 15

Thr Ala Leu Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val
 50 55 60

Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser
 65 70 75 80

Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr
145 150 155 160

His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro
260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg
290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
305 310 315 320

Asp Cys Ile Thr Lys Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg
325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln
370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn
385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu
405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro
435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp
450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg
465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg
485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn
500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser
515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro
530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met
545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu
565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln
580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp
595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln
610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His
625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His
645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu
660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu
675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg
690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe
705 710 715 720

Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu
725 730 735

Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys
740 745 750

Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr
755 760 765

Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro
770 775 780

Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile
785 790 795 800

Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn
805 810 815

Cys Phe Gly

<210> 7
 <211> 3352
 <212> DNA
 <213> Sus scrofa

<400> 7
 gagcacgaac atccttcaact gtagctgctg cccggctctgc cagccagacc ctttggagaa 60
 gaccccaactc cctgtcatgg gcccccgctg caccctgcac ccccttctc tcctggtgca 120
 ggtgacagcg ctggctgcgg ctctggccca gggcaggctg cctgccttcc tgccctgtga 180
 gctccagccc cacggcctgg tgaactgcaa ctggcttcc ctgaagtccg tgccccactt 240
 ctggcggca gcgccccggg ccaacgtcac cagcctctcc ttactctcca accgcatcca 300
 ccacctgcac gactccgact tctgtccaccc tccctggctca cgaactctca acctcaagt 360
 gaactgcccc cccggctggcc tcagccccat gcacttcccc tgccacatga ccatcgagcc 420
 caacaccccttc ctggccgtgc ccaccctggaa ggagctgaac ctgagctaca acagcatcac 480
 gaccgtgcct gcccgtcccc actccctcgat gtccctgtcg ctgagccgca ccaacatcc 540
 ggtgctagac cccacccacc tcaactggcct acatgcccctg cgctacccgt acatggatgg 600
 caactgctac tacaagaacc cctgcccagg ggccgtggag gtgggtggccgg gtggccctact 660
 cggccctgggc aacctcacac atctctcaact caagtacaac aatctcacgg aggtgcccc 720
 cagccctgccc cccagcctgg agaccctgct gtgtcctac aaccacatttgc tcaccctgac 780
 gcctgaggac ctggccaaatc tgactgcccgt ggcgtgtcgtt gatgtggggg ggaactgccc 840
 cccgctgtgac catgcccggca accccctgcag ggagtggccca aaggaccacc ccaagctgca 900
 ctctgacacc ttcagccacc tgagccgcct cgaaggccctg gtgttggaaag acagttctct 960
 ctacaacccctg gacaccagggt ggttccggagg cctggacagg ctccaaagtgc tggacccctgag 1020
 tgagaacttc ctctacgact gcatcaccaaa gaccacggcc ttccagggcc tggcccccact 1080
 ggcacccctcc tttgggcacc tccggccctt gaaggagctg gacatgcatttgc gcatcttctt 1140
 cccgctcgctc agtggagacca cgttccaaacc tctggtccaa ctgcctatgc tccagaccct 1200
 ggcgcgtgcag atgaacttca ttaaccaggc ccagctcagc atctttgggg cttccctgg 1260
 cctgtgtac gtggacccat cggacaaccg catcagcggaa gctgcaaggc cagtggccat 1320
 tactagggag gtggatggta gggagagggt ctggctgcct tccaggaacc tcgtccacg 1380
 tccactggac actctcccgct cagaggactt catgccaaac tgcaaggcct tcagcttcac 1440
 1500

cttggacctg	tctcggaaca	acctggtgac	aatccagtcg	gagatgttg	ctgcctctc	1560
acgcctcgag	tgccctgcgcc	tgagccacaa	cagcatctcc	caggcggtca	atggctctca	1620
gtttgtgccg	ctgaccagcc	tgccggtgct	ggacctgtcc	cacaacaagc	tggacctgta	1680
tcacggcgc	tagttcacgg	agctgcgcg	cctggaagca	ctggacctca	gctacaatag	1740
ccagccctt	accatgcagg	gtgtggcca	caacctcagc	ttcgtggccc	agtgcccgc	1800
cctgcgtac	ctcagcctgg	cgcacaatga	catccatagc	cgagtgtccc	agcagctctg	1860
tagcgcctca	ctgtgcgccc	tggactttag	cggaacagat	ctgagccgga	tgtggctga	1920
gggagacctc	tatctccgct	tcttccaagg	cctaagaagc	ctagtctggc	tggacctgtc	1980
ccagaaccac	ctgcacacacc	tcctgcacag	tgccctggac	aacctccccca	aaagcctgaa	2040
gcatctgcat	ctccgtgaca	ataacctggc	cttcttcaac	tggagcagcc	tgaccctcct	2100
gcccaagctg	gaaaccctgg	acttggctgg	aaaccagctg	aaggccctaa	gcaatggcag	2160
cctgccccat	ggcacccagc	tgccggaggct	ggacctcagt	ggcaacagca	tcggctttgt	2220
gaaccctggc	ttctttgccc	tggccaagca	gttagaagag	ctcaacotca	gcccataatgc	2280
cctcaagaca	gtggagccct	cctgggtttgg	ctcgatggtg	ggcaacctga	aagtccctaga	2340
cgtgagcgc	aaccctctgc	actgtgcctg	tggggcgacc	ttcgtggct	tcctgctgga	2400
ggtacaggct	gccgtgcctg	ggctgcccag	ccgcgtcaag	tgtggcagtc	cggggcagct	2460
ccaggccat	agcatctttg	cgcaagacct	gcccctctgc	ctggatgaga	ccctctcgta	2520
gaactgtttt	ggcatctcgc	tgctggccat	ggccctgggc	ctggttgtgc	ccatgctgca	2580
ccacccctgc	ggctgggacc	tctggtactg	cttccacctg	tgcctggccat	ggctgccccca	2640
ccgagggcag	cgccggggcgc	cagacgccc	gttctatgat	gccttcgtgg	tctttgacaa	2700
agctcagagt	gtctgtggccg	actgggtgta	caacgagctg	cgggtgcagc	tggaggagcg	2760
ccgtggcgc	cgcgcactgc	gcctgtgcct	ggaggagcga	gactggttac	ctggcaagac	2820
gctcttcgag	aacctgtggg	cctcagtcta	cagcagccgc	aagaccotgt	tttgctggc	2880
ccacacggac	cgtgtcagcg	gcctcttgcg	tgccagtttc	ctgctggccc	agcagcgcct	2940
gctggaggac	cgcaaggacg	ttgttagtgct	ggtgatcctg	cgtcccgatg	cctaccgctc	3000
ccgctacgtg	cggctgcgc	agcgcctctg	ccgcccagagt	gtcctccct	ggccccacca	3060
gccccgtggg	cagggcagct	tctggccca	gctgggcaca	gccctgacca	gggacaacca	3120
ccacttctat	aaccggaact	tctgcccggg	ccccacgaca	gccgaatagc	actgagtgac	3180
agcccagttg	ccccagcccc	cctggatttg	cctctctgca	tggggtgccc	caacctgctt	3240
tgctcagcca	caccactgct	ctgctccctg	ttccccaccc	caccccccag	cctggcatgt	3300

aacatgtgcc	caataaatgc	taccggaggg	ccaagaaaaaa	aaaaaaaaaa	aa	3352
<210>	8					
<211>	2457					
<212>	DNA					
<213>	Sus scrofa					
<400>	8					
atggggccccc	gctgcaccct	gcacccctt	tctctcctgg	tgcaggtgac	agcgctggct	60
gcggctctgg	cccagggcag	gctgcctgcc	ttcctgcctt	gtgagctcca	gccccacggc	120
ctggtaact	gcaactggct	cttcctgaag	tccgtgcccc	acttctcgcc	ggcagcgccc	180
cgggccaacg	tcaccagcct	ctccttactc	tccaaaccgca	tccaccacct	gcacgactcc	240
gacttcgtcc	acctgtccag	cctacgaact	ctcaacactca	agtggaaactg	cccgccggct	300
ggcctcagcc	ccatgcactt	cccctgcccac	atgaccatcg	agccaaacac	cttcctggcc	360
gtgcccaccc	tggaggagct	gaacctgagc	tacaacagca	tcacgaccgt	gcctgcctg	420
cccgactccc	tcgtgtccct	gtcgctgagc	cgcaccaaca	tcctggtgct	agacccccaco	480
cacccactg	gcctacatgc	cctgcgctac	ctgtacatgg	atggcaactg	ctactacaag	540
aaccctgccc	agggggcgct	ggaggtggtg	ccgggtgccc	tcctggccct	ggcaacacct	600
acacatctct	cactcaagta	caacaatctc	acggaggtgc	cccgacgct	gccccccagc	660
ctggagaccc	tgctgttgtc	ctacaaccac	attgtcaccc	tgacgcctga	ggacctggcc	720
aatctgactg	ccctgcgcgt	gcttgatgtg	ggggggact	gccgcgcgt	tgaccatgcc	780
cgcaacccct	cgagggagtg	cccaaaggac	caccccaagc	tgcactctga	cacccctcagc	840
cacctgagcc	gcctcgaagg	cctgggtttg	aaagacagtt	ctctctacaa	cctggacacc	900
aggtggttcc	gaggcctgga	caggctccaa	gtgctggacc	tgagtgagaa	cttcctctac	960
gactgcatca	ccaagaccac	ggcctccag	ggcctggccc	gactgcgcag	cctcaacctg	1020
tccttcaatt	accacaagaa	ggtgtccctt	gcccacctgc	acctggcacc	ctcctttggg	1080
cacctccgg	ccctgaagga	gctggacatg	catggcatct	tcttcgcgtc	gctcagttag	1140
accacgctcc	aacctctgg	ccaactgcct	atgctccaga	ccctgcgcct	gcagatgaac	1200
ttcattaacc	aggcccagct	cagcatctt	ggggcccttc	ctggcctgct	gtacgtggac	1260
ctatcgacca	accgcacatcg	cggagctgca	aggccagtg	ccattactag	ggaggtggat	1320
ggtagggaga	gggtctggct	gccttccagg	aacctcgctc	cacgtccact	ggacactctc	1380
cgctcagagg	acttcatgcc	aaactgcaag	gccttcagct	tcaccttgga	cctgtctcgg	1440
aacaacctgg	tgacaatcca	gtcgagatg	tttgctcgcc	tctcacgcct	cgagtgcctg	1500

cgcctgagcc acaacagcat	ctcccaggcg	gtcaatggct	ctcagttgt	gccgctgacc	1560
agcctgcggg	tgctggacct	gtcccacaac	aagctggacc	tgtatcacgg	1620
acggagctgc	cgcgcctgga	agcaactggac	ctcagctaca	atagccagcc	1680
cagggtgtgg	gccacaacct	cagcttcgtg	gcccagctgc	ccgcctgcg	1740
ctggcgcaca	atgacatcca	tagccgagt	tcccagcagc	tctgtagcgc	1800
gccctggact	ttagcggcaa	cgatctgagc	cggatgtggg	ctgagggaga	1860
cgcttcttcc	aaggcctaag	aagcctagtc	tggctggacc	tgtcccagaa	1920
accctcctgc	cacgtgccct	ggacaacctc	ccaaaaagcc	tgaagcatct	1980
gacaataacc	tggccttctt	caactggagc	agcctgaccc	tcctgcccaa	2040
ctggacttgg	ctggaaacca	gctgaaggcc	ctaagcaatg	gcagcctgcc	2100
cagctgcgga	ggctggacct	cagtggcaac	agcatcggt	ttgtgaaccc	2160
gccctggcca	agcagttaga	agagctcaac	ctcagcgcca	atgcctcaa	2220
ccctcctgggt	ttggctcgat	ggtggcaac	ctgaaagtcc	tagacgtgag	2280
ctgcactgtg	cctgtggggc	gacttcgtg	ggcttcctgc	tggaggtaca	2340
cctggctgc	ccagccgcgt	caagtgtggc	agtccggggc	agctccaggg	2400
tttgcgcaag	acctgcgcct	ctgcctggat	gagaccctct	cgtggaactg	2457

<210> 9
 <211> 1029
 <212> PRT
 <213> Bos taurus

<400> 9

Met	Gly	Pro	Tyr	Cys	Ala	Pro	His	Pro	Ile	Ser	Leu	Leu	Leu	Val	Gln	Ala
1					5				10					15		

Ala	Ala	Leu	Ala	Ala	Ala	Leu	Ala	Glu	Gly	Thr	Leu	Pro	Ala	Phe	Leu
								25					30		

Pro	Cys	Glu	Leu	Gln	Pro	His	Gly	Gln	Val	Asp	Cys	Asn	Trp	Leu	Phe
					35			40			45				

Leu	Lys	Ser	Val	Pro	His	Phe	Ser	Ala	Gly	Ala	Pro	Arg	Ala	Asn	Val
								55			60				

Thr	Ser	Leu	Ser	Leu	Ile	Ser	Asn	Arg	Ile	His	His	Leu	His	Asp	Ser
					65			70			75		80		

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr

305	310	315	320
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg			
325		330	335
Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His			
340	345		350
Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu			
355	360	365	
Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln			
370	375	380	
Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn			
385	390	395	400
Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu			
405	410	415	
Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro			
420	425	430	
Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu			
435	440	445	
Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp			
450	455	460	
Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn			
465	470	475	480
Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu			
485	490	495	
Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly			
500	505	510	
Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His			
515	520	525	
Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln			
530	535	540	

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr
625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu
690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val
705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile
740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg
770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
805 810 815

Phe Gly Leu Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met
820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys
835 840 845

Leu Ala His Leu Pro Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu
850 855 860

Leu Tyr Asp Ala Val Val Phe Asp Lys Val Gln Ser Ala Val Ala
865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly
885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly
900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys
915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg
930 935 940

Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp
945 950 955 960

Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr
965 970 975

Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro
980 985 990

His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Ile Ala
995 1000 1005

Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg
1010 1015 1020

Gly Pro Thr Thr Ala Glu
1025

<210> 10
<211> 818
<212> PRT
<213> Bos taurus

<400> 10

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
305 310 315 320

Asp Tyr Ile Thr Lys Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg
325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln
370 375 380

Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn
385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro

420 425 430

Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu
435 440 445Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp
450 455 460Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn
465 470 475 480Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu
485 490 495Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly
500 505 510Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His
515 520 525Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln
530 535 540Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
545 550 555 560Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
565 570 575Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
580 585 590Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
595 600 605Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
610 615 620Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr
625 630 635 640Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
 660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val
 705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
 725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
 755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
 785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
 805 810 815

Phe Gly

<210> 11
 <211> 3191
 <212> DNA
 <213> Bos taurus

<400> 11		
gggaagtggg cgccaagcat cttccctgc agtcgcctcc caacctgccc gccagaccct	60	
ctggagaagc cgcattccct gtcatggcc cctactgtgc cccgcacccc ctttctctcc	120	
tggtgcaggg ggcggcactg gcagcggccc tggccgaggg caccctgcct gccttcctgc	180	
cctgtgagct ccagcccat ggtcaggtgg actgcaactg gctgtccctg aagtctgtgc	240	
cgcacttttc ggctggagcc ccccgccca atgtcaccag ccttcctta atctccaacc	300	

gcatccacca	cttgcacatgac	tctgacttcg	tccacacctg	caacacctgcgg	gtcctcaacc	360
tcaagtgaa	ctgccccccg	gccggccctca	gccccatgca	cttccccctgc	cgtatgacca	420
tcgagccaa	caccccttcgt	gctgtgccc	ccctggagga	gctgaacactg	agctacaacg	480
gcatcacgac	cgtgcctgccc	ctgccccagtt	ccctcgtgtc	cctgtcgctg	agccacacca	540
gcatcctgg	gttagggcccc	acccacttca	ccggccctgca	cgccctgcgc	tttctgtaca	600
tggacggcaa	ctgctactac	atgaacccct	gcccgcgggc	cctggaggtg	gccccaggcg	660
ccctcctcgg	cctggggcaac	ctcacgcacc	tgtcgctcaa	gtacaacaac	ctcacggagg	720
tgcccccccg	cctgcccccc	agcctggaca	ccctgctgtc	gtcctacaac	cacattgtca	780
ccctggcacc	cgaggacctg	gccaacactga	ctgcccctgcg	cgtgcttgac	gtgggtggga	840
actgcccgg	ctgcgaccat	gcccgcacc	cctgcaggga	gtgccccaaag	aacttccccca	900
agctgcaccc	tgacacaccc	agtcacactga	gccgcctcga	aggcctggtg	ttgaaggaca	960
gttctctcta	caaactagag	aaagattgg	tccgcggcct	gggcaggctc	caagtgcgtc	1020
acctgagtga	gaacttcctc	tatgactaca	tcaccaagac	caccatctc	aacgacactga	1080
cccagctg	cagactcaac	ctgtccttca	attaccacaa	gaagggtgtcc	ttcgcacc	1140
tgcacctagc	gtcctcctt	gggagtctgg	tgtccctgga	gaagctggac	atgcacggca	1200
tcttcttccg	ctccctcacc	aacatcacgc	tccagtcgtc	gaccggctg	cccaagctcc	1260
agagtctgca	tctgcagctg	aacttcatca	accaggccc	gctcagatc	tttggggcct	1320
tcccggcct	gctcttcgtg	gacctgtcg	acaaccgc	cagcggagcc	gcgacgccag	1380
cggccgcct	gggggaggtg	gacagcagg	tgaaagtctg	gcgattgccc	aggggcctcg	1440
ctccaggccc	gctggacgc	gtcagctaa	aggacttcat	gccaagctc	aacctaact	1500
tcaccccttgg	cctgtcacgg	aacaacctgg	tgacaatcca	gcaagagatg	tttacccgc	1560
tctccgcct	ccagtgctcg	cgcctgagcc	acaacagcat	ctcgcaggcg	gttaatggct	1620
cccagttcgt	gccgctgacc	agcctgctg	tgctcgac	gtccccacaac	aagctggacc	1680
tgtaccatgg	gcgcatttc	acggagctgc	cgcagctgga	ggcactggac	ctcagctaca	1740
acagccagcc	tttcagcatg	cagggcgtgg	gccacaacct	cagcttcgtg	gcccagctgc	1800
cctccctgcg	ctacctcagc	tttgcgcaca	atggcatcca	cagccgcgtg	tcacagaagc	1860
tcagcagcgc	ctcggtgcgc	gccctggact	tcagcggcaa	ctccctgagc	cagatgtgg	1920
ccgagggaga	cctctatctc	tgcttttca	aaggcttgag	gaacctggtc	cagctggacc	1980
tgtcccgagaa	ccatctgcac	accctctgc	ctcgac	ggacaacctg	cccaagagcc	2040

tgcggcagct gcgtctccgg gacaataacc tggcttctt caactggagc agcctgaccg 2100
 tcctgccccg gctggaagcc ctggatctgg caggaaacca gctgaaggcc ctgagcaacg 2160
 gcagcctgcc gcctggcata cggctccaga agctggacgt gagcagcaac agcatggct 2220
 tcgtgatccc cggcttcttc gtccgcgcga ctcggctgat agagcttaac ctcagcgcca 2280
 atgccctgaa gacagtggat ccctccttgt tcggttcctt agcagggacc ctgaaaatcc 2340
 tagacgtgag cgccaacccg ctccactgcg cctgcggggc ggcccttgcg gacttcctgc 2400
 tggagagaca ggaggccgtg cccgggtgt ccaggcgcgt cacatgtggc agtccgggcc 2460
 agctccaggg ccgcagcata ttcacacagg acctgcgcct ctgcctggat gagaccctct 2520
 cttggactg ctttggcctc tcactgctaa tggtggcgct ggccctggca gtgcccattgc 2580
 tgcaccacct ctgtggctgg gacctcttgt actgcttcca cctgtgtctg gcccatttgc 2640
 cccgacggcg gcccgcgcg ggcgaggaca ccctgctcta tgcgtggcgtc gtggcttgc 2700
 acaaggtgca gagtgcagtg gctgattggg tgtacaacga gctccgcgtg cagctggagg 2760
 agcgcgggg ggcggggcg ctccgcctct gcctggagga gcgagactgg ctccctggta 2820
 agacgtctt cgagaacctg tgggcctcg tctacagcag ccgcaagacc atttcgtgc 2880
 tggaccacac ggaccgggtc agcggcctcc tgcgcgcag cttcctgctg gcccagcagc 2940
 gcctgttggaa ggaccgcaag gacgtcgtag tgcgtgtat cctgcgcctc gcccgcctatc 3000
 ggtcccgcta cgtgcggctg cgcgcgcgc tctgcgcgc gacgtgcctc ctctggcccc 3060
 accagcccaag tggccagggt agtttctggg ccaacctggg catagccctg accagggaca 3120
 accgtcaatt ctataaccgg aacttctgcc ggggccccac gacagccgaa tagcacagag 3180
 tgactgcccc g 3191

<210> 12
 <211> 2454
 <212> DNA
 <213> Bos taurus

<400> 12
 atggcccccactgtgcccc gcacccctt tctctctgg tgcaggcgac ggcactggca 60
 gcggccctgg ccgagggcac cctgcctgcc ttccctgcct gtgagctcca gcccattgg 120
 caggtggact gcaactggct gttccctgaag tctgtgcgc acctttcggc tggagccccc 180
 cgggccaatg tcaccagcc tcccttaatc tccaaccgca tccaccactt gcatgactct 240
 gacttcgtcc acctgtccaa cctgcgggtc ctcaacctca agtggactg cccgcggcc 300
 ggcctcagcc ccatgcactt cccctgcccgt atgaccatcg agcccaacac cttcctggct 360

gtgccaccc tggaggagct gaacctgagc tacaacggca tcacgaccgt gcctgccc	420
cccagttccc tcgtgtccct gtcgctgagc cacaccagca tcctggtgct aggccccacc	480
cacttcacccg gectgcacgc cctgcgcctt ctgtacatgg acggcaactg ctactacatg	540
aacccctgcc cgccccccct ggaggtggcc ccaggcgccc tcctcgccct gggcaaccc	600
acgcacccgt cgctcaagta caacaaccc acggaggtgc cccgcccct gccccccagc	660
ctggacaccc tgctgctgtc ctacaaccac attgtcaccc tggcacccga ggacctggcc	720
aacctgactg ccctgcgcgt gcttgacgtg ggtgggaact gcccggcgt cgaccatgcc	780
cgcaacccct gcagggagtg cccaaagaac ttcccaago tgcaccctga cacccatcgt	840
cacctgagcc gcctcgaagg cctgggttg aaggacagtt ctctctacaa actagagaaa	900
gattggttcc gccccctggg caggctccaa gtgctcgacc tgagtgagaa ctccctctat	960
gactacatca ccaagaccac catcttcaac gacctgaccc agctgcgcag actcaacctg	1020
tccttcaatt accacaagaa ggtgtccctc gcccacctgc acctagcgcc ctcccttggg	1080
agtctggtgt ccctggagaa gctggacatg cacggcatct tctccgcgtc cctcaccaac	1140
atcacgctcc agtcgctgac ccggctgccc aagctccaga gtctgcacatct gcagctgaac	1200
ttcatcaacc aggcccagct cagcatctt gggcccttc cgagccgtct cttcgtggac	1260
ctgtcgacca accgcacatcag cggagccgcg acgcccaggcc ccccccctggg ggaggtggac	1320
agcagggtgtt aagtctggcg attgcccagg ggccctcgctc caggcccgtt ggacgcccgtc	1380
agctcaaagg acttcatgcc aagctgcaac ctcaacttca cttggacccgt gtcacggAAC	1440
aacctggta caatccagca agagatgttt acccgccctt cccgcctcca gtgcctgcgc	1500
ctgagccaca acagcatctc gcaggcggtt aatggctccc agttcgctgcc gctgaccagg	1560
ctgcgagtgc tcgacccgtc ccacaacaag ctggacccgtt accatggcgct ctcattcag	1620
gagctgccgc agctggaggc actggacccgtc agctacaaca gcccggccctt cagcatgcag	1680
ggcgtggcc acaacccatcag ctgcgtggcc cagctgcctt ccctgcgtca cctcagccctt	1740
gcgcacaatg gcatccacag ccgcgtgtca cagaagctca gcagccgtcc gttgcgcgc	1800
ctggacttca gcccggcaactc cctgagccag atgtggcccg agggagacccctt ctatctctgc	1860
tttttcaaag gcttgaggaa cctgggtccag ctggacccgtt ccgagaacca tctgcacacc	1920
ctccctgcctc gtcacccgttca caacccgtcc aagagccgtc ggcagctgcg tctccgggac	1980
aataacccctgg ctttcccaa ctggagccagc ctgaccgtcc tgcccccggctt ggaagccctg	2040
gatctggcag gaaaccagct gaaggccctg agcaacggca gcctgcccggcc tggcatccgg	2100
ctccagaagc tggacccgttca cagcaacccgttcc atccgttccgc tgatccccgg ctttccgtc	2160

cgcgcgactc ggctgataga gcttaacctc agcgccaatg ccctgaagac agtggatccc 2220
 tcctggttcg gttccttagc agggaccctg aaaatcctag acgtgagcgc caacccgctc 2280
 cactgcgcct gcggggcggc ctttgtggac ttcctgctgg agagacagga ggccgtgccc 2340
 gggctgtcca ggcgcgtcac atgtggcagt ccgggccagc tccagggccg cagcatctc 2400
 acacaggacc tgcgccctcg cctggatgag accctctctt tggactgctt tggc 2454

<210> 13
 <211> 1031
 <212> PRT
 <213> Equus caballus

<400> 13

Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln
 1 . 5 10 15

Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
 35 40 . 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn
 50 55 60

Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80

Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met
 100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
 130 135 140

Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro
 145 150 155 160

Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe
260 265 270

Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe
290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu
370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly
405 410 415

Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu
420 425 430

Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu
435 440 445

Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu
450 455 460

Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
485 490 495

Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
545 550 555 560

Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser
580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe
610 615 620

Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln
645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln
675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln
690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe
705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu
740 745 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
755 760 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu
770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp
805 810 815

Asp Cys Phe Gly Leu Ser Leu Leu Val Val Ala Leu Gly Leu Ala Met
820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His
835 840 845

Leu Gly Leu Ala Trp Leu Pro Arg Arg Gly Trp Gln Arg Gly Ala Asp
850 855 860

Ala Leu Ser Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala

865	870	875	880
Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg			
885		890	895
Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu			
900	905		910
Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser			
915	920		925
Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Gln Val Ser Gly Leu			
930	935		940
Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg			
945	950	955	960
Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Ala Arg Arg Ser			
965		970	975
Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Phe			
980	985		990
Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly			
995	1000		1005
Met Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln Asn Phe			
1010	1015		1020
Cys Arg Gly Pro Thr Met Ala Glu			
1025	1030		
<210> 14			
<211> 820			
<212> PRT			
<213> Equus caballus			
<400> 14			
Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln			
1	5	10	15
Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe			
20	25		30
Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu			

35

40

45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn
50 55 60

Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
130 135 140

Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro
145 150 155 160

Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe
260 265 270

Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe
290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu
370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly
405 410 415

Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu
420 425 430

Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu
435 440 445

Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu
450 455 460

Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
485 490 495

Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
545 550 555 560

Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser
580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe
610 615 620

Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln
645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln
675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln
690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe
705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu
740 745 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
 755 760 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp
 805 810 815

Asp Cys Phe Gly
 820

<210> 15
 <211> 3391
 <212> DNA
 <213> Equus caballus

<400> 15		
ctctttctc tgagctgttg ccgcgtgaag ggactgcgag cacaaagcat cctcctctgc	60	
agctgctgcc cagtgtgcca gctggaccct ctggatcatc tcccactccc tgtcatggc	120	
ccttgcattg gtgccttgca gcccctgtct ctccctggc aggcggccat gctggccgtg	180	
gctctggccc aaggccacct gcctcccttc ctgcctgtg agctccagcc ccacggcctg	240	
gtgaactgca actggctgtt cctgaagtcc gtgccttact tctcagcagc agcaccccg	300	
gacaatgtca ccagccttcc ttgctctcc aaccgcattcc accacctcca cgactccgac	360	
tttgcccaac tgtccaaacct gcagaaactc aacctcaaat ggaactgccc gccagccggc	420	
ctcagccca tgcacttccc ctgccacatg accatcgagc ccaacacttt cctggctgta	480	
cccacccctgg aggagctgaa cctgagctac aacggcatca cgactgtgcc tgccctgccc	540	
agctccctcg tgtccctgat cctgagccgc accaacatcc tgcagctaga cccaccaggc	600	
ctcacgggcc tgcattccct gcgcttccata tacatggatg gcaactgcta ctacaagaac	660	
ccctgcgggc gggccctgga ggtggcccca ggcgcctcc ttggcctggg caacctcacc	720	
cacctgtcac tcaagtacaa caacctcaca acggtgcccc gcagcctgcc ccctagcctg	780	
gagtacctgc tttgtccta caaccacatt gtcacctgg cacctgagga cctggccat	840	
ctgactgccc tgcgtgtgct cgatgtgggt gaaaactgccc gccgctgtga ccatgcacgc	900	
aacccctgcg tggagtgccc acataaattc cccagctgc actccgacac cttagccac	960	

ctaagccgcc tagaaggcct cgtgttgaag gatagttctc tctaccagct gaaccccaga	1020
tggttccgtg gcctgggcaa cctcacagtg ctcgacctga gtgagaactt cctctacgac	1080
tgcacatcacca aaaccaaggc attccagggc ctggcccagc tgcgaaagact caacttgtcc	1140
ttcaattacc ataagaaggt gtccttcgcc cacctgacgc tggcaccctc cttcgggagc	1200
ctgctctccc tgcaggaact ggacatgcat ggcacatcttct tccgctcact cagccagaag	1260
acgctccagc cactggcccg cctgcccattg ctccagcgac tgtatctgca gatgaacttc	1320
atcaaccagg cccagctcgg catcttcaag gacttccctg gtctgcgcta catagacctg	1380
tcagacaacc gcatcagtgg agctgtggag ccgggtggca ccacaggaga ggtggatgg	1440
ggaagaagg tctggctgac atccagggac ctcactccag gcccactgga caccggcagc	1500
tctgaggact tcatgccaag ctgcaagaac ctcagcttca cttggacact gtacacggaa	1560
aacctggtaa cagtccagcc agagatgttt gcccagctct cgcgcctcca gtgcctgcgc	1620
ctgagccaca acagcatctc gcaggcggtc aatggctcac agttcgtgcc actgaccagc	1680
ctgcagggtgc tggacctgtc ccataacaaa ctggacctgt accatggcg ctcgtttacg	1740
gagctgcgc gactggaggc cctggacctc agctacaaca gccagccctt cagcatgcgg	1800
ggtgtggcc acaacctcag ctttgtggcc cagctgccc ccctgcgcta ctcagccctg	1860
gcacacaatg gcatccacag ccgtgtgtcc cagcagctct gcagcacctc gctgtggcc	1920
ctggacttca gcggcaattc cctgagccag atgtgggctg agggagacct ctatctccgc	1980
ttcttccaag gcctgagaag cctaattccgg ctagacctgt cccagaatcg tctgcataacc	2040
ctcctgcccattt gcaccctggg caacccccc aagagcttc agctgctgcg tctccgttaac	2100
aattacctgg ctttcttcaa ttggagcagc ctgaccctcc tgcccaacct ggaaaccctg	2160
gacctggctg gaaaccagct gaaggctctg agcaatggca gcctgccttc tggcacccag	2220
ctccagaggc tggacgtcag caggaacagc atcatcttcg tggcccttgg ctttttgc	2280
ctggccacga ggctgcgaga gctcaacctc agtgccaaacg ccctcaggac agaggagccc	2340
tcctggtttgc gtttccctagc aggctccctt gaagtcctag atgtgagcgc caaccctctg	2400
cactgcgcct gtggggcagc ctttgtggac ttccctgtgc aggttcaggc tgccgtgcct	2460
ggtctgccttca gccgcgtcaa gtgtggcagt ccggggccagc tccagggccg cagcatcttc	2520
gcacaagacc tgccgcctctg cctggacaag tccctctctt gggactgttt tggctctca	2580
ttgctggtttgc tggccctggg cctggccatg cctatgttgc accacctctg cggctgggac	2640
ctctggact gtttccacccctt gggccctggcc tggctgccttcc ggcgggggtg gcagcggggc	2700

gcggatgccc	ttagctatga	tgcccttgc	gtttcgaca	aggcacagag	cgcagtggcc	2760
gactgggtgt	acaatgaact	gcgggtgcgg	ctagaggagc	gccgtggcg	ccgggcgc	2820
cgcctgtgtc	tggaggagcg	tgactggcta	cctggcaaga	cgctgttgc	aaacctgtgg	2880
gcctcagtct	acagcagccg	caagatgctg	tttgtgctgg	cccacacgga	ccaggtcagt	2940
ggcctcttgc	gtgccagctt	cctgctggcc	cagcagcg	tgctggagga	ccgcaaggac	3000
gttgtggtgc	tggtaatcct	gagccctgac	gcccgccgtt	cccgtta	cggtgcgc	3060
cagcgcctct	gccgcccagag	tgtccttcc	tggccccacc	agcctagtgg	ccagcgc	3120
ttctggccc	agctaggcat	ggccctgacc	aggacaacc	gccacttcta	taaccagaac	3180
ttctggccgg	gcccgcacat	ggctgagtag	cacagagtga	cagcctggca	tgtacaaccc	3240
ccagccctga	ccttgcctct	ctgcctatga	tgcccagtct	gcctcactct	gtgacgcccc	3300
tgctctgcct	ccgcccaccc	cacccctggc	atacagcagg	cactcaataa	atgccactgg	3360
caggccaaac	agccaaaaaa	aaaaaaaaa	a			3391

<210> 16
 <211> 2460
 <212> DNA
 <213> Equus caballus

<400> 16						
atggggccctt	gocatggtgc	cctgcagccc	ctgtctctcc	tggtgcaaggc	ggccatgctg	60
gccgtggctc	tggcccaagg	caccctgcct	cccttcctgc	cctgtgagct	ccagccccac	120
ggcctggta	actgcaactg	gctgttcctg	aagtccgtgc	cccacttctc	agcagcagca	180
ccccggaca	atgtcaccag	ccttccttg	ctctccaaacc	gcatccacca	cctccacgac	240
tccgactttg	cccaactgtc	caacctgcag	aaactcaacc	tcaaatggaa	ctgcccgc	300
gccggcctca	gccccatgca	cttccctgc	cacatgacca	tgcagccaa	cacttcctg	360
gctgtaccca	ccctggagga	gctgaacctg	agctacaacg	gcatcagc	tgtgcctg	420
ctgcccagct	ccctcggtc	cctgatcctg	agccgcacca	acatcctgca	gctagacccc	480
accagcctca	cgggcctgca	tgccctgcgc	ttcctataca	tggatggcaa	ctgctactac	540
aagaacccct	gccccggggc	cctggaggtg	gccccaggcg	ccctccttgg	cctggcaac	600
ctcaccacc	tgtcactcaa	gtacaacaac	ctcacaacgg	tgcggcg	cctgccccct	660
agcctggagt	acctgctgtt	gtcctacaac	cacattgtca	ccctggcacc	tgaggac	720
gccaatctga	ctgcccctg	tgctcgat	gtgggtggaa	actgccgc	ctgtgaccat	780
gcacgcaacc	cctgcgtg	gtgcccacat	aaattccccc	agctgcactc	cgacacc	840

agccaccta gcccctaga aggctcgta ttgaaggata gttctctcta ccagctgaac 900
cccagatgtt ccgtggct gggcaaccc acagtgcgtg acctgagtga gaacttcctc 960
tacgactgca tcacccaaac caaggcattc cagggcctgg cccagctgcg aagactcaac 1020
ttgtccttca attaccataa gaaggtgtcc ttcccccacc tgacgctggc accctccctc 1080
gggagcctgc tctccctgca ggaactggac atgcattggca tcttcttccg ctcaactcagc 1140
cagaagacgc tccagccact ggcccgccctg cccatgtcc agcgtctgtt tctgcagatg 1200
aacttcatca accaggccca gctcggcatc ttcaaggact tccctggtct ggcgtacata 1260
gacctgtcag acaaccgcatt cagtggagct gtggagccgg tggccaccac aggggaggtg 1320
gatggtggga agaaggcttg gctgacatcc agggacctca ctccaggccc actggacacc 1380
cccagctctg aggacttcat gccaagctgc aagaacctca gttcacctt ggacctgtca 1440
cggaacaacc tggtaacagt ccagccagag atgtttgccc agctctcgcg cttccagtg 1500
ctgcgcctga gccacaacag catctcgcat gcggtcaatg gtcacagtt cgtgccactg 1560
accagcctgc aggtgctgga cctgtcccat aacaaactgg acctgtacca tgggcgtcg 1620
tttacggagc tgccgcact ggaggccctg gacctcagct acaacagcca gcccattcage 1680
atgcgggtg tggccacaa ctcagcttt gtggcccagc tgcccacccct gegetacctc 1740
agcctggcac acaatggcat ccacagccgt gtgtcccagc agctctcgcat cacctcgctg 1800
tggccctgg acttcagccg caattccctg agccagatgt gggctgaggg agacacttat 1860
ctccgcctt tccaaggcct gagaagccta atccggctag acctgtccca gaatcgctg 1920
cataccctcc tgccatgcac cctggcaac ctccccaaaga gttgcagct gtcgtctc 1980
cgtaacaatt acctggcctt cttcaattgg agcagcctga ccctcctgcc caacctggaa 2040
accctggacc tggctggaaa ccagctgaag gctctgagca atggcagct gccttctggc 2100
acccagctcc agaggctgga cgtcagcagg aacagcatca tttcgtggt ccctggcttc 2160
tttgcgtctgg ccacgaggct gcgagagctc aacccatgtg ccaacgcctt caggacagag 2220
gagccctcct ggtttggttt cctagcaggc tcccttgaag tcctagatgt gagcggcaac 2280
cctctgcact ggcgcctgtgg ggcagccctt gtggacttcc tgctgcaggt tcaggtgc 2340
gtgcctggtc tgcccaagccg cgtcaagtgt ggcagtcgg gccagctcca gggccgcagc 2400
atcttcgcac aagacctgca cctctgcctg gacaagtcggc tctcctggaa ctgttttgggt 2460

<210> 17
<211> 1029
<212> PRT
<213> Ovis aries

<400> 17

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
1 5 10 15

Ala Ala Leu Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
305 310 315 320

Asp Tyr Ile Thr Lys Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg
325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg
370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn
385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp
435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp
450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn
465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu
485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly .
500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr
515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln
530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr
625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu
690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val
705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile
740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg
770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
805 810 815

Phe Gly Phe Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met
820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys
835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu
850 855 860

Leu Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val Ala
865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly
885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly
900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys
915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg

930

935

940

Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp
 945 950 955 960

Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr
 965 970 975

Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro
 980 985 990

His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Met Ala
 995 1000 1005

Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg
 1010 1015 1020

Gly Pro Thr Thr Ala Glu
 1025

<210> 18
 <211> 818
 <212> PRT
 <213> Ovis aries

<400> 18

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
 1 5 10 15

Ala Ala Leu Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu
 20 25 30

Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe
 35 40 45

Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr

100

105

110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
305 310 315 320

Asp Tyr Ile Thr Lys Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg
325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg
370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn
385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp
435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp
450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn
465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu
485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly
500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr
515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln
530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr
625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu
690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val
705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile
740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg
770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
805 810 815

Phe Gly

<210> 19
 <211> 3199
 <212> DNA
 <213> Ovis aries

<400> 19						
gtcggcacgg	gaagtgagcg	ccaagcatcc	ttccctgcag	ctgcccggca	acttgcccgc	60
cagaccctct	ggagaagccg	cattccctgc	catggggccc	tactgtgccc	cgcacccct	120
ttctctcctg	gtgcaggcgg	cggcgctggc	agcagccctg	gcccaggggca	ccctgcctgc	180
cttcctgccc	tgtgagctcc	agccccgggg	taaggtgaac	tgcaactggc	tgttcctgaa	240
gtctgtgccc	cgcttttcgg	ccggagcccc	ccggggccaaat	gtcaccagcc	tctccttaat	300
ctccaaccgc	atccaccact	tgcacgactc	tgacttcgtc	cacctgtcca	acctgcgggt	360
cctcaacctc	aagtggaaact	gcccgcggc	cgccctcagc	cccatgcact	tcccctgccc	420
catgaccatc	gagcccaaca	ccttcctggc	tgtgcccacc	ctggaggagc	tgaacctgag	480
ctacaatggc	atcacgaccc	tgcctgcct	gcccagttct	ctcgtatccc	tgtcgctgag	540
ccgcaccaggc	atcctggtgc	taggccccac	ccacttcacc	ggcctgcacg	ccctgcgctt	600
tctgtacatg	gacggcaact	gctactataa	gaacccctgc	cagcaggccc	tggaggtggc	660
cccaggcgcc	ctccttggcc	tgggcaacct	cacgcacctg	tgcgtcaagt	acaacaacct	720
cacggaggtg	ccccggcgcc	tgccccccag	cctggacacc	ctgctgctgt	cctacaacca	780
catcatcacc	ctggcaccccg	aggacctggc	caatctgact	gcccctgcgt	tgcttgatgt	840
ggcgaaaaac	tgccggcgct	gcaaccacgc	ccgcaacccc	tgcagggagt	gccccaaagaa	900
cttccccaaag	ctgcacccctg	acaccttcag	ccacctgagc	cgccctcgaaag	gcctgggttt	960
gaaggacagt	tctctctaca	aactagagaa	agactggttc	cgccggctgg	gcaggctcca	1020
agtgcgtcgcac	ctgagtgaga	acttcctcta	tgactacatc	accaagacca	ccatcttcag	1080
gaacctgacc	cagctgcgca	gactcaacct	gtccttcaat	taccacaaga	agggtgcctt	1140
cgccccacctg	caactggcac	cctccttgg	gggcctggtg	tccctggaga	agctggacat	1200
gcacggcatac	ttttcccgct	ccctcaccaa	caccacgctc	cgcccgctga	cccagctgcc	1260
caagctccag	agtctgagtc	tgcagctgaa	cttcatcaac	caggccgagc	tcagcattt	1320
tggggccttc	ccgagcctgc	tcttcgtgga	cctgtcgac	aaccgcata	gcggagctgc	1380
gaggccggtg	gccgcctcg	gggaggtgga	cagcggggtg	gaagtctggc	ggtggcccag	1440

gggcctcgct ccaggccccgc tggccgcccgt cagcgcaaag gacttcatgc caagctgcaa	1500
cctcaacttc accttggacc tgtcacggaa caacctggtg acgatccagc aggagatgtt	1560
tacccgcctc tccccgcctcc agtgccctgcg cctgagccac aacagcatct cgcaggccgt	1620
taatggctcg cagttcgtgc cgctgaccccg cctgcgagtg ctcgacctgt cctacaacaa	1680
gctggacctg taccatgggc gtcgttcac ggagctgccc cagctggagg cactggacct	1740
cagctacaac agccagccct tcagcatgca gggcgtgggc cacaacctca gcttcgtggc	1800
ccagctgccc tccctgcgct acctcagcct tgccgcacaac ggcattccaca gccgcgtgtc	1860
acagaagctc agcagcgcct cgctgcgcgc cctggacttc agcggcaact ccctgagcca	1920
gatgtgggcc gagggagacc tctatctctg cttcttcaaa ggcttgagga acctgggtcca	1980
gctggacctg tccaagaacc acctgcacac cctcctgcct cgtcaccctgg ataacctgcc	2040
caagagctg cggcagctgc gtctccggga caataacctg gccttcttca actggagcag	2100
cctgactgtt ctgccccagc tggaagccct ggatctggcg ggaaaccagc tgaaggccct	2160
gagcaacggc agcctgccac ctggcaccccg gtcggagaag ctggacgtga gcagcaacag	2220
catcggtttt gtgaccctg gttttttgt ctttgcac cggctgaaag agcttaacct	2280
cagcgcacac gcccgttgaaga cagtggatcc cttctggttc ggtcgcttaa cagagaccct	2340
gaatatccta gacgtgagcg ccaacccgct coactgtgcc tgccccggc cctttgtgga	2400
cttcctgctg gagatgcagg cggccgtgcc tgggctgtcc aggccgtca cgtgtggcag	2460
tccgggccag ctccagggcc gcagcatctt cgcacaggac ctgcgcctct gcctggatga	2520
gaccctctcc ttggactgtt ttggcttctc gctgctaattt gtggcgttgg gcctggcggt	2580
gcccattgtt caccacctct gtggctggga cctgtggtaa tgcttccacc tgtgtctggc	2640
ccatttgcggc cgacggcgcc ggcagcgggg cgaggacacc ctgctctacg atgccttcgt	2700
ggtcttcgac aaggcgcaga gtgcagtggc cgactgggtg tacaacgagc tccgcgtgca	2760
gctggaggag cgccgcggc gcccggcgct ccgcctctgc ctggaggagc gagactggct	2820
ccctggcaag acgctttcg agaaccctgtg ggcctcggtc tacagcagcc gtaagaccat	2880
gttcgtgtc gaccacacgg accgggtcag tggcctctg cgcgcctgtc ttctgtggc	2940
ccagcagcgc ctgttggagg accgcaagga tgcgtggtg ctggatcc tgcgcggcc	3000
cgccatccgg tccccgtacg tgccgtgcg ccagegcctc tgccgcaga gcttcctcct	3060
ctggcccccac cagcccagtg gccaggtagt cttctggcc aacctggca tggccctgac	3120
caggacaac cgccacttct ataaccggaa cttctgcggg ggccccacga cagccgaata	3180

gcacagagtg	actgcccag	3199				
<210>	20					
<211>	2454					
<212>	DNA					
<213>	Ovis aries					
<400>	20					
atggggccct	actgtgcccc	gcacccctt	tctctcctgg	tgcagggcggc	ggcgctggca	60
gcagccctgg	cccagggcac	cctgcctgcc	ttccctgcct	gtgagctcca	gccccggggt	120
aaggtgaact	gcaactggct	gttctctgaag	tctgtgccgc	gtttttcggc	cggagcccc	180
cgggccaatg	tcaccagcct	ctccttaatc	tccaaccgca	tccaccactt	gcacgactct	240
gacttcgtcc	acctgtccaa	cctgcggggtc	ctcaacctca	agtggaaactg	cccgccggcc	300
ggcctcagcc	ccatgcactt	cccctgcccgc	atgaccatcg	agcccaacac	cttctggct	360
gtgcccaccc	tggaggagct	gaacctgagc	tacaatggca	tcacgaccgt	gcctgccttg	420
cccagttctc	tcgtatccct	gtcgctgagc	cgcaccagca	tcctggtgct	aggccccacc	480
cacttcacccg	gcctgcacgc	cctgcgttt	ctgtacatgg	acggcaactg	ctactataag	540
aacccctgcc	agcaggccgt	ggaggtggcc	ccaggcgccc	tccttggct	ggcaacctc	600
acgcacctgt	cgctcaagta	caacaacctc	acggaggtgc	cccgccgcct	gccccccagc	660
ctggacacccc	tgctgctgtc	ctacaaccac	atcatcaccc	tggcacccga	ggacctggcc	720
aatctgactg	ccctgcgtgt	gtttgatgtg	ggcgggaaact	gcccgcgtg	cgaccacgccc	780
cgcaacccct	gcagggagtg	cccaaagaac	ttccccaagc	tgcaccctga	cacccctcagc	840
cacctgagcc	gcctcgaagg	cctgggtttg	aaggacagtt	ctctctacaa	actagagaaa	900
gactggttcc	gccccctggg	caggctccaa	gtgctcgacc	tgagtgagaa	cttcctctat	960
gactacatca	ccaagaccac	catcttcagg	aacctgaccc	agctgcgcag	actcaacctg	1020
tccttcaatt	accacaagaa	ggtgtccctc	gcccacctgc	aactggcacc	ctccttgggg	1080
ggcctgggtgt	ccctggagaa	gctggacatg	cacggcatct	tcttcgcctc	cctcaccaac	1140
accacgctcc	ggccgctgac	ccagctgccc	aagctccaga	gtctgagtct	gcagctgaac	1200
ttcatcaacc	aggccgagct	cagcatctt	ggggccttcc	cgagcctgtct	cttcgtggac	1260
ctgtcggaca	accgcatcag	cggagctgctg	aggccgggtgg	ccgcccctcg	ggaggtggac	1320
agcgggggtgg	aagtctggcg	gtggcccagg	ggcctcgctc	caggcccgt	ggccgcccgtc	1380
agcgcaaagg	acttcatgccc	aagctgcaac	ctcaacttca	ccttggaccc	gtcacggaac	1440
aacctggta	cgatccagca	ggagatgttt	acccgcctct	cccgccctcca	gtgcctgcgc	1500

ctgagccaca acagcatctc gcagggcggtt aatggctgc agtgcgtgcc gctgacccgc	1560
ctgcgagtgc tcgacacctgc ctacaacaag ctggacacctgt accatggcg ctcgttcacg	1620
gagctgccgc agctggaggc actggacacctc agctacaaca gccagccctt cagcatgcag	1680
ggcgtgggcc acaacacctcag cttcggtggcc cagctgccgt ccctgcgcta cctcagccctt	1740
gcgcacaacg gcatccacag ccgcgtgtca cagaagctca gcagccctc gctgcgcgcc	1800
ctggacttca gcggcaactc cctgagccag atgtggcccg agggagacct ctatctctgc	1860
ttcttcaaag gcttgaggaa cctggtccag ctggacacctgt ccaagaacca cctgcacacc	1920
ctcctgcctc gtcacaccttgc taacctgccc aagagcctgc ggcagctgcg tctccgggac	1980
aataacctgg ctttcttcaa ctggagcagc ctgactgttc tgccccagct ggaagccctg	2040
gatctggcg gaaaccagct gaaggccctg agcaacggca gcctgcacc tggcacccgg	2100
ctccagaagc tggacgtgag cagcaacagc atcggctttg tgacccttgg cttctttgtc	2160
cttgccaaacc ggctgaaaga gcttaacctc agcgccaaacg ccctgaagac agtggatccc	2220
ttctggttcg gtcgcttaac agagaccctg aatatcctag acgtgagcgc caacccgctc	2280
cactgtgcct gcggggcgcc ctttgtggac ttccctgctgg agatgcaggc ggccgtgcct	2340
gggctgtcca ggcgcgtcac gtgtggcagt ccggggccagc tccaggcccg cagcatttc	2400
gcacaggacc tgcgcccttg cctggatgag accctcttctt tggactgctt tgg	2454

<210> 21

<211> 1032

<212> PRT

<213> *Canis familiaris*

<400> 21

Met	Gly	Pro	Cys	Arg	Gly	Ala	Leu	His	Pro	Leu	Ser	Leu	Leu	Val	Gln
1															15

Ala	Ala	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Gln	Gly	Thr	Leu	Pro	Ala	Phe
20															30

Leu	Pro	Cys	Glu	Leu	Gln	Pro	His	Gly	Leu	Val	Asn	Cys	Asn	Trp	Leu
35															45

Phe	Leu	Lys	Ser	Val	Pro	Arg	Phe	Ser	Ala	Ala	Pro	Arg	Gly	Asn
50														

Val	Thr	Ser	Leu	Ser	Leu	Tyr	Ser	Asn	Arg	Ile	His	His	Leu	His	Asp
65															80

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
145 150 155 160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe
260 265 270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe
290 295 300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu
370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu
385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu
420 425 430

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val
435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly
450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp
465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg
485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln
500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu
515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr
530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro

545 550 555 560

Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu
565 570 575

Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg
580 585 590

Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser
595 600 605

Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg
610 615 620

Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn
625 630 635 640

Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser
645 650 655

Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp
660 665 670

Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly
675 680 685

Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln
690 695 700

Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro
705 710 715 720

Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala
725 730 735

Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly
740 745 750

Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys
755 760 765

Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro
770 775 780

Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly
785 790 795 800

Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu
805 810 815

Ser Trp Val Cys Phe Ser Leu Ser Leu Ala Val Ala Leu Ser Leu
820 825 830

Ala Val Pro Met Leu His Gln Leu Cys Gly Trp Asp Leu Trp Tyr Cys
835 840 845

Phe His Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly
850 855 860

Val Asp Ala Leu Ala Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
865 870 875 880

Ser Ser Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu
885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp
900 905 910

Trp Val Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr
915 920 925

Ser Ser Arg Lys Thr Leu Phe Val Leu Ala Arg Thr Asp Arg Val Ser
930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Cys Pro Asp Ala His
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln
995 1000 1005

Leu Gly Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln
1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Thr Ala
1025 1030

<210> 22
<211> 822
<212> PRT
<213> Canis familiaris

<400> 22

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Pro Arg Gly Asn
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
145 150 155 160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe
260 265 270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe
290 295 300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu
370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu
385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu
420 425 430

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val
435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly
450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp
465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg
485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln
500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu
515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr
530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro
545 550 555 560

Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu
565 570 575

Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg
580 585 590

Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser
595 600 605

Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg
610 615 620

Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn
625 630 635 640

Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser
645 650 655

Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp

660

665

670

Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly
 675 680 685

Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln
 690 695 700

Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro
 705 710 715 720

Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala
 725 730 735

Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly
 740 745 750

Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys
 755 760 765

Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro
 770 775 780

Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly
 785 790 795 800

Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu
 805 810 815

Ser Trp Val Cys Phe Ser
 820

<210> 23
 <211> 3334
 <212> DNA
 <213> Canis familiaris

<400> 23
 aggaaggggc tggagactcc aagcatacctt tccctgcagct gctgcccagc ctggcagcc 60
 gaccctctgg agaagccccc gctccctgtc atggggccctt gccgtggcgc cctgcacccc 120
 ctgtctctcc tgggtgcaggc tgccgcgccta gccctggccc tggcccaggc caccctgcct 180
 gccttcctgc cctgtgagct ccagccccat ggcctggtga actgcaactg gctgttcctc 240
 aagtccgtgc cccgcttctc ggcagctgca ccccgcggtta acgtcaccag cctttccttg 300

tactccaacc	gcatccacca	cctccatgac	tatgactttg	tccacttcgt	ccacacctgcgg	360
cgtctcaatc	tcaagtggaa	ctgcccgc	cccagcctca	gccccatgca	ctttccctgt	420
cacatgacca	ttgagccaa	caccccttg	gctgtgccc	ccctagagga	cctgaatctg	480
agctataaca	gcatcacgac	tgtgcccgc	ctgcccagtt	cgcttgtgtc	cctgtccctg	540
agccgcacca	acatcctgg	gctggaccct	gccaccctgg	caggcctta	tgcctgcgc	600
ttcctgttcc	tggatggcaa	ctgctactac	aagaacccct	gccagcaggc	cctgcagg	660
gccccaggtg	ccctcctggg	cctggcaac	ctcacacacc	tgtcactcaa	gtacaacaac	720
ctcaccgtgg	tgccgcgggg	cctgcccccc	agcctggagt	acctgctt	gtcctacaac	780
cacatcatca	ccctggcacc	tgaggacctg	gcaatctga	ctgcctgcg	tgcctcgat	840
gtgggtggga	actgtcgccg	ctgtgaccat	gcccgtaacc	cctgcagg	gtgccc	900
ggcttccccc	agctgcaccc	caacaccc	ggccacctga	gccacctcg	aggectgg	960
ttgagggaca	gctctctcta	cagcctggac	cccaggtgg	tccatgg	ggcaac	1020
atgggtctgg	acctgagtga	gaacttctg	tatgactgca	tcacaaa	caaagc	1080
tacggcctgg	cccggtcg	cagactcaac	ctgccttca	attatcataa	gaagg	1140
tttgc	ccacc	tgcac	atcctcttca	gggagcctac	tgc	1200
atacatggca	tcttcttccg	ctcgctc	aagaccacgc	tccagtcg	ggcccac	1260
cccatgctcc	agcgtctgca	tctgc	aactttatca	gccagg	ccatc	1320
ttcggcgc	tccctggact	gcccgt	gacttgc	acaacc	catc	1380
gcagagcc	cggt	gcccac	aggggagg	gagg	gtgt	1440
cagtccccc	accttgc	ggcccact	ggcac	gctc	aggc	1500
agctgcagga	ccctcaactt	caccc	ctgtctcg	acaac	ctgt	1560
ccggagatgt	ttgtccgg	ggcg	cagt	gcct	gagcc	1620
tcgcaggcgg	tcaatgg	gcag	tctg	cct	tgc	1680
tcccataaca	agctgg	acc	gtacc	cc	cggt	1740
gccttggacc	tca	atgg	cgcc	cc	gtgg	1800
agcttgtgg	cacag	ctg	cc	cc	gac	1860
agccgcgtgt	ccc	aggc	cc	cc	tt	1920
accctgagcc	agatgtgg	cgagg	cc	cc	tt	1980
agcctgg	ttc	agg	cc	cc	cc	2040
gacaac	ccaa	agg	cc	cc	cc	2100

aactggagca	gcctggccct	cctacccaag	ctggaaagccc	tggacctggc	gggaaaccag	2160
ctgaaggccc	ttagcaatgg	cagcttgc	cc aacggcaccc	agctccagag	gctggac	2220
agcggcaaca	gcacatcg	cggtcccc	agctttttg	ccctggccgt	gaggc	2280
gagctcaacc	tca	gccc	taaag	acgg	ttgg	2340
gcgggtgccc	tgaa	agtc	ccat	tgca	ttgc	2400
ac	ttcg	tgtgg	tttgc	ggagg	cggtgc	2460
aagtgcggca	gcccgg	ccca	gtcc	ccaggc	cgac	2520
tgcc	ctgg	acgt	ccat	tcg	acag	2580
agc	cgg	ccat	tcgt	ccat	ccat	2640
ctgt	ccat	tgcc	ccat	cgct	gtgc	2700
gac	ccat	ttcg	ttcg	ccat	gtgt	2760
ctg	ccat	ttcg	ttcg	ccat	ggat	2820
cgt	ccat	ttcg	ttcg	ccat	gtgc	2880
cc	ccat	ttcg	ttcg	ccat	ccat	2940
ttc	ccat	ttcg	ttcg	ccat	gtgt	3000
ctgt	ccat	ttcg	ttcg	ccat	gtgt	3060
agt	ccat	ttcg	ttcg	ccat	ggat	3120
acgg	ccat	ttcg	ttcg	ccat	ccat	3180
acag	ccat	ttcg	ttcg	ccat	ttcg	3240
ggat	ccat	ttcg	ttcg	ccat	ccat	3300
taa	ccat	ttcg	ttcg	ccat	ttcg	3334

<210> 24
 <211> 2466
 <212> DNA
 <213> *Canis familiaris*

<400> 24	atggggccct	gcgtggcg	cctgcacccc	ctgtctctcc	tggtgcaaggc	tgccgcgcta	60	
	gccc	tggccc	caccc	cctgc	gccttc	cctgtgagct	ccagccccat	120
	ggc	cgtgt	actg	caactg	gctgtt	cactgc	cccgcttctc	180
	cccc	cggt	acgt	caccag	cctt	ccttgc	gtatccacca	240
	tatgactt	tg	ccacttc	gt	ccac	ctgcgg	cgtctcaatc	300

gccagcctca	gccccatgca	cttccctgt	cacatgacca	ttgagccaa	cacccctcg	360
gctgtgccc	ccctagagga	cctgaatctg	agctataaca	gcatcacgac	tgtgcccgc	420
ctgcccagtt	cgcttgtgtc	cctgtccctg	agccgcacca	acatcctgg	gctggaccct	480
gccaccctgg	caggccttta	tgccctgcgc	ttcctgttcc	tggatggcaa	ctgctactac	540
aagaacccct	gccagcaggc	cctgcaggtg	gccccaggtg	ccctcctggg	cctgggcaac	600
ctcacacacc	tgtcactcaa	gtacaacaac	ctcaccgtgg	tgccgcgggg	cctgcccccc	660
agcctggagt	acctgcttt	gtcctacaac	cacatcatca	ccctggcacc	tgaggacctg	720
gccaatctga	ctgcccctg	tgtcctcgat	gtgggtggga	actgtcgcgg	ctgtgaccat	780
gcccgttaacc	cctgcagggg	gtgccccaaag	ggcttccccc	agctgcaccc	caacacccctc	840
ggccacctga	gccacctcga	aggcctggtg	ttgagggaca	gctctctcta	cagcctggac	900
cccaggtgg	tccatggcct	ggcaacctc	atggtgctgg	acctgagtga	gaacttcctg	960
tatgactgca	tcacccaaac	caaagccttc	tacggcctgg	cccgctgcg	cagactcaac	1020
ctgtccttca	attatcataa	gaagggtgtcc	tttgcacc	tgcacatggc	atcctccttc	1080
gggagcctac	tgtccctgca	ggagctggac	atacatggca	tcttctccg	ctogctcagc	1140
aagaccacgc	tccagtcgt	ggcccacctg	cccatgctcc	agcgtctgca	tctgcagttg	1200
aactttatca	gccaggcccc	gctcagcata	ttcggcgcct	tccctggact	gcggtaacgt	1260
gacttgcag	acaaccgcata	cagtggagct	gcagagcccg	cggctgccac	aggggaggt	1320
gaggcagact	gtggggagag	agtctggcca	cagtcccg	accttgcct	ggggccactg	1380
ggcacccccc	gctcagaggg	cttcatgccc	agctgcagga	ccctcaactt	cacccctggac	1440
ctgtctcgga	acaacctagt	gactgtcag	ccggagatgt	ttgtccggct	ggcgccctc	1500
cagtgcctgg	gcctgagcca	caacagcata	tcgcaggcgg	tcaatggctc	gcagttcgt	1560
cctctgagca	acctgcgggt	gctggacctg	tcccataaca	agctggacct	gtaccacggg	1620
cgctcggtca	cgagctgccc	gcccgtggag	gccttgacc	tcaatggctc	gcagttcgt	1680
ttcagcatgc	ggggcgtggg	ccacaatctc	agctttgtgg	cacagctgcc	agccctgcgc	1740
tacctcagcc	tggcgcacaa	tggcatccac	agccgcgtgt	cccagcagct	ccgcagcgcc	1800
tcgctccggg	ccctggactt	cagtggcaat	accctgagcc	agatgtggc	cgagggagac	1860
ctctatctcc	gtttttcca	aggcctgaga	agccctggtc	agctggacct	gtcccagaat	1920
cgcctgcata	ccctcctgccc	acgcaacctg	gacaacctcc	ccaagagcct	gcggctcctg	1980
cggctccgtg	acaattacct	ggctttcttc	aactggagca	gcctggccct	cctacccaag	2040

ctggaaagccc tggacacctggc gggaaaccag ctgaaggccc tgagcaatgg cagcttgccc 2100
 aacggcaccc agctccagag gctggacctc agcggcaaca gcatcggttt cgtggtcccc 2160
 agcttttttgc ccctggccgt gaggcttcga gagctcaacc tcagcgccaa cgccctcaag 2220
 acggtgaggc cctcctgggtt tggttccctg gcgggtgccc tgaaagtccct agacgtgacc 2280
 gccaaccctt tgcattgcgc ttgccccgca accttcgtgg acttcttgct ggaggtgcag 2340
 gctgcgggtgc ccggcctgcc tagccgtgtc aagtgcggca gcccgggcca gctccaggc 2400
 cgcacatct tcgcacagga cctgcgcctc tgccctggacg aagcgccttc ctgggtctgt 2460
 ttcagc 2466

<210> 25
 <211> 1031
 <212> PRT
 <213> Felis catus

<400> 25

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
 20 25 30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
 100 105 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
 130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe
260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe
290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu
370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu
420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu
435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu
450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser
485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser
580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe

610 615 620

Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg
645 650 655

Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
660 665 670

Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln
675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln
690 695 700

Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe
705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
725 730 735

Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu
740 745 750

Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala
755 760 765

Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
770 775 780

Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
805 810 815

Asp Cys Phe Gly Leu Ser Leu Leu Thr Val Ala Leu Gly Leu Ala Val
820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His
835 840 845

Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Gly Ala Asp
 850 855 860

Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala
 865 870 875 880

Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg
 885 890 895

Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu
 900 905 910

Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser
 915 920 925

Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu
 930 935 940

Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg
 945 950 955 960

Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His Arg Ser
 965 970 975

Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu
 980 985 990

Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly
 995 1000 1005

Thr Ala Leu Thr Arg Asp Asn Gln His Phe Tyr Asn Gln Asn Phe
 1010 1015 1020

Cys Arg Gly Pro Thr Thr Ala Glu
 1025 1030

<210> 26
 <211> 820
 <212> PRT
 <213> Felis catus

<400> 26

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe
260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe
290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Ala Phe Gln Gly Leu Ala Gln Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu
370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu
420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu
435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu
450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser
485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser
580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe
610 615 620

Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg
645 650 655

Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
660 665 670

Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln
675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln
690 695 700

Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe
705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala

725

730

735

Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu
740 745 750

Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala
755 760 765

Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
770 775 780

Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
805 810 815

Asp Cys Phe Gly
820

```
<210> 27
<211> 3235
<212> DNA
<213> Felis catus
```

<400> 27
agggtctgcg agctccaggc attcttctct gccatcgctg cccagtctgc catccagacc 60
ctctggagaa gcccccaactc cctgtcatgg gcccctgcca tggcgccctg caccggctgt 120
ctctccttgt gcagggtcgcc ggcgtggccg tggccctggc ccagggcacc ctgcctgcct 180
ttctgccttg tgagctccag cgccacggcc tggtaattt cgactggctg ttccctcaagt 240
ccgtgccccca cttctcgccg gcagcgcccc gtggtaacgt caccagcctt tccctgtact 300
ccaaacggcat ccaccaccc tcacgactccg actttgtcca cctgtccagc ctgcggcg 360
tcaacctcaa atgaaactgc ccacccgcca gcctcagccc catgcacttc ccctgtcaca 420
tgaccattga gccccacacc ttccctggccg tgcccacccct ggaggagctg aacctgagct 480
acaacagcat cacgacagta cccggccctgc ccagttccct cgtgtccctg tccttgagcc 540
gtaccaacat cctggtgctg gaccctgcca acctcgcagg gctgcactcc ctgcgtttc 600
tgttccttggaa tggcaactgc tactacaaga accccctgccc gcaggccctg caggtggccc 660
cgggcgccct ctttggcctg ggcaacctta cgcacccgtc actcaagtac aacaacccat 720
ctgcggtgcc ccggggcctg ccccccagcc tggagttaccc gctattgtcc tacaaccaca 780

tcatcacccct	ggcacctgag	gacctggcca	acctgaccgc	cctgcgtgt	ctcgatgtgg	840
gtgggaactg	ccgtcgctgt	gaccacgccc	gcaacccctg	tatggagtgc	cccaagggct	900
tcccgacac	ctgac	acccctgac	acccctgac	acctgaacca	cctcgaaggc	960
aggacagctc	tctctacaac	ctgaacccca	gatggttcca	tgccctggc	aacctcatgg	1020
tgctggac	cttgcataat	actgcataac	caaaaccaca	gccttccagg	1080	
gcctggccca	gctgcgcaga	ctcaacttgt	ctttcaatta	ccacaagaag	gtgtcctttg	1140
ccacactgca	tctggcgccc	tccttcggg	gcctgcgttc	cctgcagcag	ctggacatgc	1200
atggcatctt	cttccgctcg	ctcagcgaga	ccacgctccg	gtcgctggc	cacctggccca	1260
tgctccagag	tctgcacctg	cagatgaact	tcatcaatca	ggcccagctc	agoatcttcg	1320
gggccttccc	tggcctgcga	tacgtggacc	tgtcagacaa	ccgcataagt	ggagccatgg	1380
agctggcg	tgccacgggg	gagggtggatg	gtggggagag	agtccggctg	ccatctgggg	1440
acctagctct	gggcccaccc	ggcaccccta	gctccgaggg	cttcatgcca	ggctgcaaga	1500
ccctcaactt	cacccctggac	ctgtcacgga	acaacctagt	gacaatccag	ccagagatgt	1560
ttgcccggct	ctcgccctc	cagtgcctgc	tcctgagccg	caacagcatc	tcgcaggcag	1620
tcaacggctc	acaattttatg	ccgctgacca	gcctgcaggt	gctggacctg	tccataaca	1680
agctggac	gtaccatggg	cgctcttca	cgaggctgccc	cgggctggag	gccctggacc	1740
tca	ccatccaa	cagccagccc	ttcagcatgc	agggcgtggg	tcacaacctc	1800
ccatccaa	cacatccaa	tatctcagcc	tggcgcacaa	cgacatccac	agccgtgtgt	1860
ccatccaa	ctgcagcgcc	tcgctgcggg	ccttggactt	cagcggcaat	gccttgagcc	1920
ccatccaa	cgatgtggc	cgagggagac	ctgtatctcc	acttcttccg	aggcctgagg	1980
ccatccaa	gtcccagaat	cgccctgcata	ccctcttgcc	acgcacccctg	gacaacctcc	2040
ccatccaa	gcccgtgctg	cgtctccgtg	acaatttatct	ggctttcttc	aactggagca	2100
ccatccaa	cctcccccagg	ctggaagccc	tggacctggc	ggaaaccag	ctgaaggccc	2160
ccatccaa	tgagcaacgg	cagcttgcct	aatggaaccc	agctccagag	gctggacctc	2220
ccatccaa	gtatcagctt	cgtggcctcc	agcttttttgc	ctctggccac	caggctgcga	2280
ccatccaa	tcagtgccaa	cgccctcaag	acgggtggagc	cctccctggtt	cggttctcta	2340
ccatccaa	tgaaagtcc	agatgtgact	ggcaacccccc	tgcactgcgc	ctgtggggcg	2400
ccatccaa	acttcttgct	ggaggtgcag	gctgcagtgc	ccggcctgccc	aggccacgtc	2460
ccatccaa	gtccaggta	gctccagggc	cgcagcatct	ttgcgcagga	tctgcgcctc	2520
ccatccaa	aggccctctc	ctgggactgt	tttggcctct	cgctgcgtac	cgtggccctg	2580

tgcccatgct gcaccaccc tcgtggctggg acctctggta ctgtttccac ctgtgcctgg	2640
cctggctgcc ccggcggggg cgccggcggg gcgcggatgc cctgcctac gatgcctttg	2700
tggtcttcga caaggcacag agcgccgtgg ccgactgggt gtacaacgag ctgcgggtac	2760
ggctagagga gcccgtgga cgcggagcgc tccgcctgtg cctggaggaa cgtgactggc	2820
tacccggtaa aacgctcttt gagaacctgt gggcctcagt ttacagcagc cgcaagatgc	2880
tgtttgtgct gccccacaca gacagggtca gccgccttgc gcgccagc tttctgctgg	2940
cccaggcagcg cctgctggag gaccgcaagg acgttgtggt gctggtgatc ctgcggcccg	3000
acgcccaccc ctcccgctat gtgcggctgc gccagcgcct ctgcggccag agcgtccctcc	3060
tctggccccca ccagcccagt ggccagcgc gcttctggc ccagctggc acggccctga	3120
ccagggacaa ccagcacttc tataaccaga acttctgccc gggccccacg acggcagagt	3180
gaccgccccag caccctaaagc ctcctacacc ttgcctgtct gcctggatg ccggg	3235

<210> 28
 <211> 2460
 <212> DNA
 <213> *Felis catus*

<400> 28	
atggggccctt gccatggcgc cctgcacccc ctgtctctcc tgggtgcaggc tgccgcgcgt	60
gcccgtggccc tggcccaggg caccctgcct gcctttctgc cctgtgagct ccagcgccac	120
ggcctggta attgcgactg gctgttcctc aagtccgtgc cccacttctc ggccggcagcg	180
ccccgtggta acgtcaccag cttttccctg tactccaacc gcatccacca cctccacgac	240
tccgactttg tccacctgtc cagccgtcgg cgtctcaacc tcaaattggaa ctgccccaccc	300
gccagcctca gccccatgca cttccctgt cacatgacca ttgagcccc caccttcctg	360
gcccgtgccc ccctggagga gctgaacctg agctacaaca gcatcacgac agtacccgccc	420
ctgcccagtt ccctcggtc cctgtccttg agccgtacca acatcctggt gctggaccct	480
gccaacctcg cagggctgca ctccctgcgc tttctgttcc tggatggcaa ctgtactac	540
aagaaccctt gccccgaggc cctgcaggtg gccccggggcg ccctccttgg cctgggcaac	600
cttacgcacc tgcactcaa gtacaacaac ctcactgcgg tgccccgcgg cctggccccc	660
agcctggagt acctgctatt gtcctacaac cacatcatca ccctggcacc tgaggacctg	720
gccaacctga ccgcctgcg tgcgtcgat gtgggtggga actgcgtcg ctgtgaccac	780
gccccgcaacc cctgtatgga gtgccccaaag ggcttccgc acctgcaccc tgacacacctc	840
agccacacctga accacacctga aggcctggtg ttgaaggaca gctctctcta caacacctgaac	900

cccaagatgg	tccatgc	ccc	ggcaac	ctc	atgg	tgctgg	ac	ctg	agt	ga	gaa	ttc	c	ta	960					
tat	gact	tgca	tcac	ccaa	aa	ac	ca	gc	c	tt	gg	cc	c	tt	1020					
tt	gt	ttt	ca	attac	ca	ca	ga	ag	gt	tg	cc	ac	c	tt	1080					
gg	ga	gc	c	tgc	ca	gc	ag	ct	gg	ac	cc	c	tc	tc	1140					
gag	acc	ac	gc	tcc	g	tc	cc	gt	cc	at	gg	ca	tt	cc	1200					
aact	tc	at	ca	atc	agg	ccc	ca	gt	cc	ttt	cc	cc	tc	ac	gt	1260				
gac	ct	gt	tc	ag	ac	cc	ca	at	gg	ag	ct	gg	cc	ac	gg	tg	1320			
gat	gg	gt	gg	gg	ag	ag	at	cc	gt	cc	at	ct	gg	cc	cc	ac	gg	gg	1380	
cct	ag	ct	cc	cg	gg	ct	cc	at	tc	cc	tt	cc	tc	tc	gt	ca	1440			
cg	ga	ac	aa	cc	ac	aa	cc	ct	ca	ac	tt	cc	tc	gt	gt	ca	1500			
ct	g	ct	ct	ga	cc	at	cc	ca	at	tc	cc	cc	tc	cg	ct	gt	1560			
acc	ag	cc	ct	gc	ag	at	ttt	gccc	gg	ct	tc	cc	cc	c	tc	gt	1620			
ttc	ac	cg	gg	ag	gg	gg	gg	cc	ct	cc	at	cc	cc	cc	cc	ac	cc	gg	1680	
at	gc	ag	gg	cc	gg	gg	gg	cc	at	tc	cc	cc	cc	cc	cc	cc	cc	at	tc	1740
agc	ct	gg	gc	gc	cc	ac	at	cc	cc	at	tc	cc	cc	cc	cc	cc	cc	cc	cc	1800
cgg	cc	tt	gg	gg	cc	tt	gg	gg	cc	at	tc	cc	cc	cc	cc	cc	cc	cc	cc	1860
ct	cc	ac	tt	tc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1920
cata	cc	ct	ct	tg	cc	ac	gc	ac	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1980
cgt	gaca	att	at	tc	gg	cc	tt	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	2040
gccc	tgg	gg	acc	tt	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	2100
accc	ag	gg	ct	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	2160
ttt	gt	ct	gg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	2220
gag	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	2280
ccc	ct	gc	act	gt	gg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	2340
gt	gg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	2400
at	ctt	tg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	2460

<210> 29 .
 <211> 1032
 <212> PRT
 <213> Mus musculus

<400> 29

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn
50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn
65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met
100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro
180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu

225	230	235	240
Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg			
245	250	255	
Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser			
260	265	270	
Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly			
275	280	285	
Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe			
290	295	300	
Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu			
305	310	315	320
Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu			
325	330	335	
Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala			
340	345	350	
Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu			
355	360	365	
Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu			
370	375	380	
Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met			
385	390	395	400
Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala			
405	410	415	
Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr			
420	425	430	
Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu			
435	440	445	
Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser			
450	455	460	

Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu
465 470 475 480

Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
485 490 495

Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp
515 520 525

Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
545 550 555 560

Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser
565 570 575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val
580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly
595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe
610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu
645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr
660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn
675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly
755 760 765

Ala Ala Phe Val Asp Leu Leu Glu Val Gln Thr Lys Val Pro Gly
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser
805 810 815

Trp Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Met Val
820 825 830

Val Pro Ile Leu His His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe
835 840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Ala Arg Ser Arg Arg Ser
850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu
885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp
900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser
930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
980 985 990

Leu Phe Trp Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln
995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln
1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu
1025 1030

<210> 30
<211> 821
<212> PRT
<213> Mus musculus

<400> 30

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ser Cys Ser Asn
50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn
65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met
100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro
180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser
260 265 270

Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe
290 295 300

Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu
325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala

340

345

350

Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu
355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu
370 375 380

Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala
405 410 415

Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr
420 425 430

Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu
435 440 445

Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser
450 455 460

Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu
465 470 475 480

Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
485 490 495

Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp
515 520 525

Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
545 550 555 560

Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser
565 570 575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val
580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly
595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe
610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu
645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr
660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn
675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly
755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser
805 810 815

Trp Asp Cys Phe Gly
820

<210> 31
 <211> 3200
 <212> DNA
 <213> Mus musculus

<400> 31						
tgtcagaggg	agcctcgaaa	gaatccctcca	tctcccaaca	tggttctccg	tcaaggact	60
ctgcacccct	tgtccctcct	ggtacaggct	gcagtgctgg	ctgagactct	ggccctgggt	120
accctgcctg	ccttcctacc	ctgtgagctg	aaggctcatg	gcctggtgga	ctgcaattgg	180
ctgttcctga	agtctgtacc	ccgtttctct	gcggcagcat	cctgctccaa	catcaccgc	240
ctctccttga	tctccaaaccg	tatccaccac	ctgcacaact	ccgacttcgt	ccacctgtcc	300
aacctgcggc	agctgaacct	caagtggAAC	tgtccacccaa	ctggccttag	ccccctgcac	360
ttctcttgcc	acatgaccat	tgagcccaga	accttcctgg	ctatgcgtac	actggaggag	420
ctgaacctga	gctataatgg	tatcaccact	gtgccccgac	tgcccagctc	cctggtaat	480
ctgagcctga	gccacaccaa	catcctgggt	ctagatgcta	acagcctcgc	cggcctatac	540
agcctgcgcg	ttctcttcat	ggacgggaac	tgctactaca	agaacccctg	cacaggagcg	600
gtgaaggtga	ccccaggcgc	cctcctgggc	ctgagcaatc	tcacccatct	gtctctgaag	660
tataacaacc	tcaccaaagg	gccccccaa	ctgccccca	gcctggagta	cctcctggtg	720
tcctataacc	tcattgtcaa	gctggggct	gaagacctgg	ccaatctgac	ctcccttcga	780
gtacttgatg	tgggtggaa	ttgcccgtgc	tgcgaccatg	cccccaatcc	ctgtatagaa	840
tgtggccaaa	agtccctcca	cctgcacccct	gagaccttcc	atcacctgag	ccatctggaa	900
ggcctggtgc	tgaaggacag	ctctotccat	acactgaact	cttcctggtt	ccaaggtctg	960
gtcaacctct	cggtgctgga	cctaagcgcg	aactttctct	atgaaagcat	caaccacacc	1020
aatgccttcc	agaacctaac	ccgcctgcgc	aagctcaacc	tgtcctcaa	ttaccgcaag	1080
aaggatccct	ttgcccgcct	ccacctggca	agttccttca	agaacctggt	gtcactgcag	1140
gagctgaaca	tgaacggcat	tttctccgc	tcgctcaaca	agtacacgct	cagatggctg	1200
gccgatctgc	ccaaactccaa	cactctgcatt	cttcaaattga	acttcataaa	ccaggcacag	1260
ctcagcatct	ttggcacctt	ccgagccctt	cgctttgtgg	acttgcaga	caatgcatac	1320
agtggccctt	caacgctgtc	agaagccacc	cctgaagagg	cagatgatgc	agagcaggag	1380
gagctgttgt	ctgcggatcc	tcacccagct	ccactgagca	ccccctgcttc	taagaacttc	1440

atggacaggt gtaagaactt caagttcacc atggacctgt ctcggaacaa cctggtgact	1500
atcaagccag agatgttgtt caatctctca cgcctccagt gtcttagcct gagccacaac	1560
tccattgcac aggctgtcaa tggctctcag ttccctgccgc tgactaatct gcaggtgctg	1620
gacctgtccc ataacaaact ggacttgtac cactggaaat cgttcagtga gctaccacag	1680
ttgcaggccc tggacctgag ctacaacagc cagccctta gcatgaaggg tataggccac	1740
aatttcagtt ttgtggccca tctgtccatg ctacacagcc ttgcctggc acacaatgac	1800
attcataccct gttgtcctc acatctcaac agcaactcag tgaggttct tgacttcagc	1860
ggcaacggta tggggccgcat gtggatgag gggggcctt atctccattt cttccaaggc	1920
ctgagtgccc tgctgaagct ggacctgtct caaaataacc tgcatatcct ccggccccag	1980
aaccttgaca acctccccaa gagcctgaag ctgctgagcc tccgagacaa ctacctatct	2040
ttcttaact ggaccagtct gtccttcctg cccaacctgg aagtccataga cctggcaggc	2100
aaccagctaa aggccctgac caatggcacc ctgcctaattg gcaccctcct ccagaaactg	2160
gatgtcagca gcaacagtat cgtctctgtg gtcccagcct tcttcgtct ggccgtcgag	2220
ctgaaagagg tcaacctcag ccacaacatt ctcaagacgg tggatcgctc ctggtttggg	2280
cccatgtga tgaacctgac agttcttagac gtgagaagca accctctgca ctgtgcctgt	2340
ggggcagcct tcgttagactt actgttggag gtgcagacca aggtgcctgg cctggctaat	2400
ggtgtgaagt gtggcagccc cggccagctg cagggccgta gcatcttcgc acaggacctg	2460
cggctgtgcc tggatgaggt cctctttgg gactgccttg gccttcact cttggctgt	2520
gccgtggca tggtggtgcc tatactgcac catctctgct gctggacgt ctggactgt	2580
tttcatctgt gcctggcatg gctaccttg ctggcccgca gcccacgcag cgcccaagct	2640
ctcccctatg atgccttcgt ggtgttcgt aaggcacaga ggcgcgttgc ggactgggt	2700
tataacgagc tgcgggtgcg gctggaggag cggcgccgac gcccacacgg acgctgtgt	2760
ctggaggacc gagattggct gcctggccag acgccttcgt agaacctctg ggcttccatc	2820
tatggagcc gcaagactct atttgtgctg gcccacacgg accgcgtcag tggcttcctg	2880
cgcaccagct tcctgctggc tcagcagcgc ctgttggaaag accgcaagga cgtgggtgg	2940
ttgggtatcc tgcgtccgga tgcccacccgc tcccgctatg tgcgcactgcg ccagcgtctc	3000
tgccgccaga gtgtgctctt ctggcccccag cagcccaacg ggcagggggg ctctggcc	3060
cagctgagta cagccctgac tagggacaac cgccacttct ataaccagaa ctctgcgg	3120
ggacctacag cagaatagct cagagcaaca gctggaaaca gctgcacattt catgcctgg	3180
tcccgagttg ctctgcctgc	3200

<210> 32
 <211> 2463
 <212> DNA
 <213> *Mus musculus*

<400> 32
 atggttctcc gtcgaaggac tctgcacccc ttgtccctcc tggcacaggc. tgcagtgcgt 60
 gctgagactc tggccctggg taccctgcct gccttcctac cctgtgagct gaagcctcat 120
 ggcctgggtgg actgcaattg gctgtccctg aagtctgtac cccgttctc tgccggcagca 180
 tcctgctcca acatcaccgg cctctcccttgc atctccaacc gtatccacca cctgcacaac 240
 tccgacttcg tccacactgtc caacctgcgg cagctgaacc tcaagtgaa ctgtccaccc 300
 actggccta gccccctgca cttctcttgc cacatgacca ttgagcccag aaccttcctg 360
 gctatgcgta cactggagga gctgaacctg agctataatg gtatcaccac tgtgccccga 420
 ctgcccagct ccctgggtgaa tctgagcctg agccacacca acatcctggt tctagatgct 480
 aacagcctcg cccgcctata cagcctgcgc gttctcttca tggacgggaa ctgctactac 540
 aagaacccct gcacaggagc ggtgaaggtg accccaggcg ccctcctggg cctgagcaat 600
 ctcacccatc tgtctctgaa gtataacaac ctcacaaaagg tgccccgcca actgcccccc 660
 agcctggagt acctcctggt gtcctataac ctcattgtca agctggggcc tgaagacctg 720
 gccaatctga cctcccttcg agtacttgat gtgggtgggaa attgccgtcg ctgcgaccat 780
 gcccccaatc cctgtataga atgtggccaa aagtccctcc acctgcaccc tgagaccttc 840
 catcacctga gccatctgga aggcctggtg ctgaaggaca gctctctcca tacactgaac 900
 tcttcctggt tccaagggtct ggtcaacctc tcgggtgtgg acctaagcga gaactttctc 960
 tatgaaagca tcaaccacac caatgcctt cagaacctaa cccgcctgcg caagctcaac 1020
 ctgtccttca attaccgcaa gaaggatatcc tttgcccccc tccacctggc aagttccttc 1080
 aagaacctgg tgtcaactgca ggagctgaac atgaacggca tcttcttccg ctcgctcaac 1140
 aagtacacgc tcagatggct ggccgatctg cccaaactcc acactctgca tcttcaaattg 1200
 aacttcatca accaggcaca gtcagcatc tttggtacct tccgagccct tcgccttgc 1260
 gacttgcag acaatcgcat cagtggccct tcaacgctgt cagaagccac ccctgaagag 1320
 gcagatgatg cagagcagga ggagctgttg tctgcggatc ctcacccagc tccactgagc 1380
 acccctgctt ctaagaactt catggacagg tgtaagaact tcaagttcac catggacctg 1440
 tctcggaaca acctggtgac tatcaagcca gagatgtttg tcaatctctc acgcctccag 1500
 tgtcttagcc tgagccacaa ctccattgca caggctgtca atggctctca gttccctgccc 1560

ctgactaatac	tgcaggtgct	ggacctgtcc	cataacaaac	tggacttgta	ccactggaaa	1620
tcgttcagtg	agctaccaca	gttcaggcc	ctggacctga	gctacaacag	ccagcccttt	1680
agcatgaagg	gtataggcca	caatttcagt	tttggcc	atctgtccat	gctacacagc	1740
cttagcctgg	cacacaatga	cattcatacc	cgtgtgtcct	cacatctcaa	cagcaactca	1800
gtgaggtttc	ttgacttcag	cggcaacgg	atggggcgca	tgtggatga	ggggggcctt	1860
tatctccatt	tcttccaagg	cctgagtggc	ctgctgaagc	tggacctgtc	tcaaaataac	1920
ctgcataatcc	tccggcccca	gaaccttgac	aacctccccca	agagcctgaa	gctgctgagc	1980
ctccgagaca	actacctatc	tttcttaac	tggaccagtc	tgtccttcct	gcccaacctg	2040
gaagtccat	acctggcagg	caaccagcta	aaggccctga	ccaatggcac	cctgccta	2100
ggcacccctcc	tccagaaact	ggatgtcagc	agcaacagta	tctgtctgt	ggtcccagcc	2160
ttcttcgctc	tggcggtcga	gctgaaagag	gtcaacctca	gccacaacat	tctcaagacg	2220
gtggatcgct	cctggtttgg	gcccattgtg	atgaacctga	cagttctaga	cgtgagaagc	2280
aaccctctgc	actgtgcctg	tggggcagcc	ttcgttagact	tactgttgg	ggtgcagacc	2340
aaggtgcctg	gcctggctaa	tggtgtgaag	tgtggcagcc	ccggccagct	gcagggccgt	2400
agcatcttcg	cacaggacct	gcccgtgtc	ctggatgagg	tctctcttg	ggactgcttt	2460
ggc						2463

<210> 33
 <211> 1032
 <212> PRT
 <213> Homo sapiens

<400> 33

Met	Gly	Phe	Cys	Arg	Ser	Ala	Leu	His	Pro	Leu	Ser	Leu	Leu	Val	Gln
1						5			10					15	

Ala	Ile	Met	Leu	Ala	Met	Thr	Leu	Ala	Leu	Gly	Thr	Leu	Pro	Ala	Phe
		20					25						30		

Leu	Pro	Cys	Glu	Leu	Gln	Pro	His	Gly	Leu	Val	Asn	Cys	Asn	Trp	Leu
		35				40					45				

Phe	Leu	Lys	Ser	Val	Pro	His	Phe	Ser	Met	Ala	Ala	Pro	Arg	Gly	Asn
		50			55				60						

Val	Thr	Ser	Leu	Ser	Leu	Ser	Ser	Asn	Arg	Ile	His	His	Leu	His	Asp
65					70				75				80		

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser
130 135 140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser
145 150 155 160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe
260 265 270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe
290 295 300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu

305	310	315	320
Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu			
325	330	335	
Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala			
340	345	350	
His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu			
355	360	365	
Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu			
370	375	380	
Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met			
385	390	395	400
Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly			
405	410	415	
Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu			
420	425	430	
Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu			
435	440	445	
Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu			
450	455	460	
Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser			
465	470	475	480
Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser			
485	490	495	
His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val			
500	505	510	
Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu			
515	520	525	
Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu			
530	535	540	

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly
545 550 555 560

Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr
565 570 575

Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser
580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe
610 615 620

Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln
645 650 655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser
660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg
675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg
690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe
705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu
740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
805 810 815

Asp Cys Phe Ala Leu Ser Leu Leu Ala Val Ala Leu Gly Leu Gly Val
820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His
835 840 845

Leu Cys Leu Ala Trp Leu Pro Trp Arg Gly Arg Gln Ser Gly Arg Asp
850 855 860

Glu Asp Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Thr Gln
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Gly Gln Leu Glu
885 890 895

Glu Cys Arg Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp
900 905 910

Trp Leu Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser
930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Gly Arg
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln
995 1000 1005

Leu Gly Met Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg
1010 1015 1020

Asn Phe Cys Gln Gly Pro Thr Ala Glu
1025 1030

<210> 34
<211> 820
<212> PRT
<213> Homo sapiens

<400> 34

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn
50 55 60

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser
130 135 140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser
145 150 155 160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe
260 265 270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe
290 295 300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu
325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala
340 345 350

His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu
370 375 380

Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu

420

425

430

Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu
435 440 445

Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu
450 455 460

Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
485 490 495

His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu
515 520 525

Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly
545 550 555 560

Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr
565 570 575

Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser
580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe
610 615 620

Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln
645 650 655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser
 660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg
 675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg
 690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe
 705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
 725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu
 740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
 755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
 805 810 815

Asp Cys Phe Ala
 820

<210> 35
 <211> 3352
 <212> DNA
 <213> Homo sapiens

<400> 35
 aggctggat aaaaatctta cttcctctat tctctgagcc gctgctgccc ctgtggaaag 60
 ggacctcgag tgtgaagcat cttccctgt agctgctgtc cagtctgccc gccagaccct 120
 ctggagaagc ccctgcccc cagcatgggt ttctgccgca ggcgcctgca cccgctgtct 180
 ctcctgggtgc aggccatcat gctggccatg accctggccc tgggtacctt gcctgccttc 240
 ctaccctgtg agctccagcc ccacggcctg gtgaactgca actggctgtt cctgaagtct 300

gtgccccact tctccatggc	360
agcaccccggt ggcaatgtca	
ccagccttc cttgtcctcc	
aaccgcatcc accacctcca	420
tgattctgac tttgcccacc	
tgcccagcct gggcatctc	
aacctcaagt ggaactgccc	480
gccgggttggc ctcagccca	
tgcacttccc ctgccacatg	
accatcgagc ccagcacctt	540
cttggctgtg cccaccctgg	
aagagctaaa cctgagctac	
aacaacatca tgactgtgcc	600
tgcgctgccc aaatccctca	
tatccctgtc cctcagccat	
accaacatcc tgatgctaga	660
ctctgccagc ctcgcccggcc	
tgcatgccc gcgcttcata	
ttcatggacg gcaactgtta	720
ttacaagaac ccctgcaggc	
aggcactgga ggtggccccc	
ggtgccctcc ttggcctggg	780
caacctcacc cacctgtcac	
tcaagtacaa caacctcact	
gtgggtcccc gcaacctgcc	840
ttccagcctg gagtatctgc	
tgttgtccca caacccgatc	
gtcaaactgg cgccctgagga	900
cctggccaaat ctgaccgccc	
tgcgtgtgct cgatgtggc	
ggaaattgcc gccgctgcga	960
ccacgctccc aacccctgca	
tggagtgccc tcgtcacttc	
ccccagctac atcccgatac	1020
cttcagccac ctgagccgtc	
ttgaaggcct ggtgttgaag	
gacagttctc ttcctggct	1080
aatgcccagt tggttccgtg	
ggctggaaaa cctccgagtg	
ctggacctga gtgagaactt	1140
cctctacaaa tgcataacta	
aaaccaaggc cttccaggc	
ctaacacagc tgcgcaagct	1200
taacctgtcc ttcaattacc	
aaaagagggt gtcctttgcc	
cacctgtctc tggcccttcc	1260
tttcggagc ctggtcgccc	
tgaaggagct ggacatgcac	
ggcatcttct tccgctca	1320
cgatgagacc acgctccggc	
cactggcccg cctgcccatt	
ctccagactc tgcgtctgca	1380
gatgaacttc atcaaccagg	
cccagctcgg catcttcagg	
gcctccctg gcctgcgcta	1440
cgtggacctg tcggacaacc	
gcatcagcgg agcttcggag	
ctgacagcca ccatggggga	1500
ggcagatgga ggggagaagg	
tctggctgca gcctggggac	
cttgcctccg ccccagtgg	1560
cactcccagc tctgaagact	
tcaggccaa ctgcagcacc	
ctcaacttca cttggatct	1620
gtcacggAAC aacctggta	
ccgtgcagcc ggagatgttt	
gcccagctct cgcacctgca	1680
gtgcctgcgc ctgagccaca	
actgcatactc gcaggcagtc	
aatggctccc agttcctgcc	1740
gctgaccgggt ctgcaggtgc	
tagacctgtc ccgcaataag	
ctggacctct accacgagca	1800
ctcattcactc gagctaccgc	
gactggaggc cctggacctc	
agctacaaca gccagccctt	1860
tggcatgcag ggcgtggcc	
acaacttcag cttcgtggct	
cacctgcgca ccctgcgcca	1920
cctcagccctg gcccacaca	
acatccacag ccaagtgtcc	
cagcagctct gcagtagcgt	1980
gctgcgggcc ctggacttca	
gcggcaatgc actggccat	
atgtggcccg agggagacct	2040
ctatctgcac ttcttccaag	
gcctgagcgg ttgtatctgg	

ctggacttgt	cccagaaccg	cctgcacacc	ctcctgcccc	aaaccctgcg	caacccccc	2100
aagagcctac	aggtgctgcg	tctccgtgac	aattacctgg	ccttctttaa	gtggtggagc	2160
ctccacttcc	tgcccaaact	ggaagtccctc	gacctggcag	gaaaccggct	gaaggccctg	2220
accaatggca	gcctgcctgc	tggcacccgg	ctccggaggc	tggatgtcag	ctgcaacagc	2280
atcagcttcg	tggcccccgg	cttctttcc	aaggccaagg	agctgcgaga	gctcaacctt	2340
agcgccaacg	ccctcaagac	agtggaccac	tcctggtttgc	ggcccccggc	gagtgcctg	2400
caaatactag	atgttaagcgc	caaccctctg	caactgcgcct	gtgggggggc	ctttatggac	2460
ttcctgctgg	aggtgcagggc	tgccgtgccc	ggtctgccc	gccgggtgaa	gtgtggcagt	2520
ccggggccagc	tcaggggcct	cagcatctt	gcacaggacc	tgcgcctctg	cctggatgag	2580
gccctctcct	gggactgttt	cgcctctcg	ctgctggctg	tggctctggg	cctgggtgtg	2640
cccatgctgc	atcacctctg	tggctggac	ctctggtaact	gtttccacct	gtgcctggcc	2700
tggctccct	ggcgaaaaacg	gcaaaagtggg	cgagatgagg	atgcctgccc	ctacgatgcc	2760
ttcgtggct	tcgacaaaac	gcagagcgc	gtggcagact	gggtgtacaa	cgagcttcgg	2820
gggcagctgg	aggagtgcgc	tggcgctgg	gcactccgccc	tgtgcctgga	ggaacgcgc	2880
tggctgcctg	gaaaaaccct	ctttgagaac	ctgtggccct	cggctatgg	cagccgcaag	2940
acgctgttttgc	tgctggccca	cacggaccgg	gtcagtggtc	tctgcgcgc	cagttccctg	3000
ctggcccagc	agcgccctgc	ggaggaccgc	aaggacgtcg	tgggtctgg	gatcctgagc	3060
cctgacggcc	gccgctcccg	ctacgtgcgg	ctgcgcctgc	gcctctgccc	ccagagtgtc	3120
ctcctctggc	cccaccagcc	cagtggtcag	cgcagcttct	gggcccagct	ggcatggcc	3180
ctgaccaggaa	acaaccacca	cttctataac	cgaaacttct	gccagggacc	cacggccgaa	3240
tagccgtgag	ccggaatcct	gcacggtgcc	acccacac	tcacccatccc	tctgcctgcc	3300
tggtctgacc	ctccccctgct	cgcctccctc	accccacacc	tgacacagag	ca	3352

<210> 36
 <211> 2460
 <212> DNA
 <213> Homo sapiens

<400> 36	atgggtttct	gccgcagcgc	cctgcaccccg	ctgtctctcc	tgggtcagggc	catcatgctg	60
	gccatgaccc	tggccctggg	taccttgccc	gccttcctac	cctgtgagct	ccagccccac	120
	ggcctggta	actgcaactg	gctgttcctg	aagtctgtgc	cccacttctc	catggcagca	180
	ccccgtggca	atgtcaccag	cctttccctg	tcctccaacc	gcatccacca	cctccatgat	240

tctgactttg cccacctgcc cagccctgccc catctcaacc tcaagtggaa ctgccccccg	300
gttggcctca gccccatgca cttccctgc cacatgacca tcgagcccag caccttcttg	360
gctgtgccccca cccttggaaaga gctaaacctg agctacaaca acatcatgac tgtgcctgccc	420
ctgccccaaat ccctcatatc cctgtccctc agccataccca acatcctgat gctagactct	480
gccagccctcg ccggcctgca tgccttgcgc ttccatttca tggacggcaa ctgttattac	540
aagaacccct gcaggcaggc actggaggtg gccccgggtg ccctccttgg cctgggcaac	600
ctcacccacc tgtcactcaa gtacaacaac ctcactgtgg tgccccgcaa cctgccttcc	660
agcctggagt atctgctgtt gtcctacaac cgcacatgtca aactggcgcc tgaggacctg	720
gccaatctga ccggcctgccc tgtgctcgat gtggggggaa attggccggc ctgcgaccac	780
gctcccaacc cctgcatttgcgt gtgcctcgat cacttcccc agctacatcc cgatacccttc	840
agccacccatgca gccgttgcgttga aggccctgggtg ttgaaggaca gttctcttc ctggctgaat	900
gccagttgggt tccgtgggct gggaaacctc cgagtgtgg acctgagtga gaacttcctc	960
tacaaatgca tcaactaaac caaggcccttc cagggcctaa cacagctgccc caagcttaac	1020
ctgtccttca attaccaaaa gagggtgtcc tttgcccacc tgtctctggc cccttccttc	1080
gggagcctgg tccgcctgaa ggagctggac atgcacggca tcttcttccg ctcactcgat	1140
gagaccacgc tccggccact ggcccgcctg cccatgtcc agactctgccc tctgcagatg	1200
aacttcatca accaggccca gtcggcattc ttcaggccct tccctggccct ggcgtacgt	1260
gacctgtcgg acaaccgcatt cagcggagct tcggagctga cagccaccat gggggaggca	1320
gatggagggg agaaggctcg gctgcagccct ggggaccttg ctccggcccc agtggacact	1380
cccaagctctg aagacttcag gccaactgc agcaccctca acttcacccctt ggatctgtca	1440
cggaacaacc ttgtgaccgt gcagccggag atgtttgccca agctctcgca cctgcagtg	1500
ctgcgcctga gccacaactg catctcgccag gcagtcaatg gctccagtt cctgcgcgtg	1560
accggctctgc aggtgctaga cctgtcccgca aataagctgg acctctacca cgagcactca	1620
ttcacggagc taccgcgact ggaggccctg gacctcagct acaacagcca gccctttggc	1680
atgcagggcg tgggccacaa cttcagcttc gtggctcacc tgcgcaccct gcccaccc	1740
agcctggccc acaacaacat ccacagccaa gtgtcccagc agctctgcag tacgtcgctg	1800
cgggcccctgg acttcagccgg caatgcactg ggccatatgt gggccgaggg agacctctat	1860
ctgcacttct tccaaggccct gaggcggttg atctggctgg acttgcacccca gaaccgcctg	1920
cacacccctcc tgccccaaac cctgcgcacac cttcccaaga gcctacaggt gctgcgtctc	1980
cgtgacaatt acctggccctt ctttaagtgg tggagccctcc acttcctgccc caaactggaa	2040

gtcctcgacc tggcagaaaa cccgctgaag gccctgacca atggcagcct gcctgctggc 2100
acccggctcc ggaggctgga tgtcagctgc aacagcatca gcttcgtggc ccccggttc 2160
ttttccaagg ccaaggagct gcgagagctc aaccttagcg ccaacgcctt caagacagt 2220
gaccactcct gtttgggccc cctggcgagt gccctgcaaa tactagatgt aagcgccaa 2280
cctctgcact gcgcctgtgg ggccgccttt atggacttcc tgctggaggt gcaggctgcc 2340
gtgcccggtc tgcccagccg ggtgaagtgt ggcagtccgg gccagctcca gggcctcagc 2400
atcttgcac aggacctgcg cctctgcctg gatgaggccc tctcctgggatctgttcgccc 2460

<210> 37
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 37
accttgcctg ctttcctacc ctgtga 26

<210> 38
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 38
gtccgtgtgg gccagcacaa a 21

<210> 39
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 39
tccatgacgt ttttgatgtt 20

<210> 40
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 40
tccataacgt ttttcatgtt 20

<210> 41
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 41
tccatcacgt ttttcatgtt 20

<210> 42
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 42
tccattacgt ttttcatgtt 20

<210> 43
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 43
tccatggcgt ttttcatgtt 20

<210> 44
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 44
tccatgccgt ttttcatgtt 20

<210> 45
<211> 20
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 45

tccatgtcgt ttttcatgtt

20

<210> 46

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 46

tccatgtatgt ttttcatgtt

20

<210> 47

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 47

tccatgaagt ttttcatgtt

20

<210> 48

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 48

tccatgaggt ttttcatgtt

20

<210> 49

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 49

tccatgacat ttttcatgtt

20

<210> 50

<211> 20

<212> DNA

<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 50
tccatgacct ttttgatgtt 20

<210> 51
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 51
tccatgactt ttttgatgtt 20

<210> 52
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 52
tccatgacgc ttttgatgtt 20

<210> 53
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 53
tccatgacga ttttgatgtt 20

<210> 54
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 54
tccatgacgg ttttgatgtt 20

<210> 55
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 55
tccatgacgt ctttgatgtt

20

<210> 56
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 56
tccatgacgt atttgatgtt

20

<210> 57
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 57
tccatgacgt gtttgatgtt

20

<210> 58
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 58
tcgtcgaaaa gtcgttttgtt cgtt

24

<210> 59
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 59
tgctgaaaaa gtgcttttgtt gctt

24

<210> 60
<211> 20
<212> DNA

<213> Artificial sequence
<220>
<223> Synthetic oligonucleotide

<400> 60
tccatgacgt tcctgatgct

20

<210> 61
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 61
tccatgagct tcctgatgct

20

<210> 62
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Consensus oligopeptide

<220>
<221> MISC_FEATURE
<222> (4)...(5)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (7)...(12)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (14)...(15)
<223> Any amino acid

<400> 62

Gly Asn Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
1 5 10 15

<210> 63
<211> 16
<212> PRT
<213> Homo sapiens

<400> 63

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys
1 5 10 15

<210> 64
<211> 16
<212> PRT
<213> Mus musculus

<400> 64

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Ile Cys
1 5 10 15

<210> 65
<211> 31
<212> PRT
<213> Artificial sequence

<220>
<223> Consensus oligopeptide

<220>
<221> MISC_FEATURE
<222> (2)..(8)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (14)..(22)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (25)..(30)
<223> Any amino acid

<400> 65

Arg Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Asp Xaa Tyr Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Ser Xaa Xaa Xaa Xaa Xaa Tyr
20 25 30

<210> 66
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (2)..(8)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (14)..(22)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (25)..(30)
<223> Any amino acid

<400> 66

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Xaa Xaa Xaa Xaa Xaa Tyr
20 25 30

<210> 67
<211> 31
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (2)..(8)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (14)..(22)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (25)..(30)
<223> Any amino acid

<400> 67

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Gln Leu Xaa Xaa Xaa Xaa Xaa Xaa Tyr
20 25 30

<210> 68
<211> 31
<212> PRT
<213> Homo sapiens

<400> 68

Gln Val Leu Asp Leu Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His
1 5 10 15

Ser Phe Thr Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr
20 25 30

<210> 69
<211> 31
<212> PRT
<213> Mus musculus

<400> 69

Gln Val Leu Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys

1

5

10

15

Ser Phe Ser Glu Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr
20 25 30

<210> 70
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 70
tccaggactt ctctcaggtt 20